

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:01:21 ; Search time 72.54 Seconds  
(without alignments)  
32.830 Million cell updates/sec

Title: US-08-833-506c-25

Perfect score: 103

Sequence: 1 GIVPFRSFQQRLHDSQH 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16.\*

1: sp\_bacteria.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phage.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_unclassified.\*

13: sp\_vertebrate.\*

14: sp\_virus.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	99	96.1	1114	4	094994
2	99	96.1	1147	11	09R0W4
3	99	96.1	1147	11	09QW28
4	90	87.4	82	6	09TTT6
5	89	86.4	945	6	09N175
6	89	86.4	1154	6	097604
7	76	73.8	366	6	09N176
8	75	72.8	1206	11	09WTK6
9	74	71.8	1127	13	09PU92
10	73	70.9	306	11	09JTV7
11	71	68.9	1205	6	09RUX8
12	56	54.4	1206	5	077104
13	56	54.4	1349	5	09VKP8
14	51	49.5	255	10	042697
15	51	49.5	320	10	09S9E0
16	51	49.5	346	10	041641
17	49	47.6	146	6	09N127
18	49	47.6	267	2	09RAY1
19	48	46.6	605	2	032214

20	48	46.6	507	2	09KF76	09kf76 bacillus ha
21	47	45.6	614	2	09R0X4	09kux4 vibrio chol
22	47	45.6	699	10	048938	048938 petroselinu
23	47	45.6	705	10	024425	024425 eschscholzi
24	46	44.7	506	10	096560	096560 helianthus
25	46	44.7	583	3	09US28	09us28 schizosacch
26	46	44.7	588	10	096561	096561 helianthus
27	46	44.7	604	2	09JUD8	09jud8 neisseria m
28	46	44.7	604	2	09JUD8	09jud8 neisseria m
29	46	44.7	622	3	09HE34	09he34 neurospora
30	46	44.7	656	10	09FVM7	09fvm7 triticum ae
31	46	44.7	692	10	043235	043235 vicia sativ
32	46	44.7	704	10	004434	004434 pisum sativ
33	46	44.7	711	10	09SUM3	09sum3 arabidopsis
34	46	44.7	712	10	09SUM3	09sum3 arabidopsis
35	45	43.7	582	5	09VSJ5	09vsj5 drosophila
36	45	43.7	5149	2	09I179	09i179 pseudomonas
37	44	42.7	89	2	09KDP3	09kdp3 bacillus ha
38	44	42.7	567	10	09SW40	09sw40 arabidopsis
39	44	42.7	683	10	024424	024424 papaver som
40	44	42.7	692	1	09HRL3	09hrl3 halobacteri
41	44	42.7	692	10	09R035	09r035 arabidopsis
42	44	42.7	692	10	09SB48	09sb48 arabidopsis
43	43	41.7	217	2	09I334	09i334 pseudomonas
44	43	41.7	326	5	018648	018648 caenorhabdi
45	43	41.7	612	2	09PD80	09pd80 xylella fas

## ALIGNMENTS

RESULT 1

094994 ID 094994 PRELIMINARY; PRT; 1114 AA.

AC 094994;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE INDUCIBLE NITRIC OXIDE SYNTHASE.

GN INOS.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Ogawa Y., Nishijima S., Goto M., Ida M.;

"Cloning and characterization of a novel splice variant of human

RT inducible nitric oxide synthase."

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB022318; BAA37123.1;

DR HSSP; P35228; 4NOS.

DR InterPro; IPR001094;

DR InterPro; IPR001433;

DR InterPro; IPR001709;

DR Pfam; PF00175; oxidored\_fad; 1.

DR Pfam; PF00667; FAD\_binding; 1.

DR PRINTS; PR00369; FLAVODOXIN.

DR PRINTS; PR00371; FPNCR.

SQ SEQUENCE 1114 AA; 126748 MW; C1F9624774435571 CRC64;

Query Match 96.1%; Score 99; DB 4; Length 1114;

Best Local Similarity 94.4%; Pred. No. 2.7e-08;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVPFRSFQQRLHDSQH 18

|| |||||

Db 946 GIAPFRSFQQRLHDSQH 963

RESULT 2

DT		01-MAR-2001 (TrEMBLrel_16, Last annotation update)
DE	CYTOKINE INDUCIBLE NITRIC OXIDE SYNTHASE, INOS.	
OS	Rattus sp.	
OC	Eukaryota; Metazoa;	
CC	Mammalia; Eutheria;	
OX	NCHI_TaxID=10118;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=G3221515; PubMed=7682072;	
RA	Wood E.R., Berger H.Jr., Sherman P.A., Lapetina E.G.;	
RT	"Hepatocytes and macrophages express an identical cytokine inducible	
RL	nitric oxide synthase gene.";	
RS	Biochem. Biophys. Res. Commun. 191:767-774(1993).	
HSP:	P29477; INOS.	
IPI:	-	
IPR:	IPR001094;	
INTP:	IPR001433;	
INTERP:	IPR001709;	
INTRP:	IPR002369;	
INTEPR:	IPR003097;	
IFAM:	PF001175; oxidored_fad; 1.	
FPAM:	PF00667; FAD_binding; 1.	
PRINTS:	PRO0369; FLAVODOXIN.	
PRINTS:	PRO0371; FPNCR.	
PRODOM:	PD001811;-; 1.	
SQ	SEQUENCE 1147 AA; 130635 MW; 2CAFV9B93E5F651A CRC64;	
Query Match	96.1%; Score 99; DB 11; Length 1147;	
Best Local Similarity	94.4%; Pred.No. 2.7e-08;	
Matches	1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 GVPSFRSQWQRHLDSQH 18 	
Dd	982 GIAPFSRWQLRHLSQH 999 	
RESULT 4		
ID Q9TTT6 PRELIMINARY; PRD 82 AA.		
AC OSTT6		
DT 01-MAY-2000 (TrEMBLrel_13, Created)		
DT 01-MAY-2000 (TrEMBLrel_13, Last sequence update)		
DE 01-MAR-2001 (TrEMBLrel_16, Last annotation update)		
DE INDUCIBLE NITRIC OXIDE SYNTHASE NOS2 (FRAGMENT).		
OS Orcytolagus cuniculus (Rabbit).		
OC Eukaryota; Metazoa;		
CC Mammalia; Eutheria;		
OX NCBI_TaxID=9986;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=NEW ZEALAND WHITE; TISSUE=KIDNEY;		
RA Tsao L.S., O'Brien W.J.;		
RN Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.		
RT		
RC SEQUENCE FROM N.A.		
RC STRAIN=NEW ZEALAND WHITE; TISSUE=HEART MYOCARDIUM;		
RX PubMed=11053770;		
RA Shi Y., Pritchard K.A., Baker J.E.;		
RT "Chronic myocardial hypoxia increases nitric oxide synthase and		
RL decreases caveolin-3";		
RL Free Radic. Biol. Med. 29:695-703(2000).		
DR EMBL; AF198443; AAF09500.1; -.		
DR EMBL; AF200351; AAG24286.1; -.		
DR HSSP; P00388; IAMO		
DR InterPro; IPR001709; -.		
DR PRINTS; PRO0371; FPNCR.		
FT NON_TER 1		
FT TER 82		
SQ SEQUENCE 82 AA; 9396 MW; 73244479A4B965F6 CRC64;		
Query Match	87.4%; Score 90; DB 6; Length 82;	
Best Local Similarity	83.3%; Pred.No. 5.9e-08;	

DR InterPro; IPR001433; -;

RN [1]

```
Qy 1 GIVPFRSEWQQR LHD 15
    || |||||: ||
Db 982 GIAPFRSEWQOOFHD 996
```

RESULT	11	
Q9TUX8		
ID	Q9TUX8	PRELIMINARY; PRT; 1205 AA.
AC	Q9TUX8;	
DT	01-MAY-2000 (TReMBLrel. 13, Created)	
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)	
DT	01-OCT-2000 (TReMBLrel. 15, Last annotation update)	
DE	NITRIC OXIDE SYNTHASE.	
DE	NITRIC OXIDE SYNTHASE.	
GN	NOS.	
OS	Canis familiaris (Dog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	
OX	NCBI_TaxID=9615;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
TX	TISSUE=HEART;	
RC	MEDLINE=99369487; PubMed=10442857;	
RA	Schwemmer M., Bassege E.;	
RT	*Assembly and characterization of canine heart endothelial nitric	
RT	oxide synthase cDNA and 5'-flanking sequence by homology (RT-PCR)	
RT	cloning.";	
RL	Nitric Oxide 3:254-264(1999).	
DR	EMBL; AF143503; AAD52161.1; -.	
DR	HSSP; P29474; 3NOS.	
DR	InterPro; IPR001094; -.	
DR	InterPro; IPR001433; -.	
DR	InterPro; IPR001709; -.	



```

DR InterPro: IPR003097; -.
DR Pfam: PF00175; oxidored_fad; 1.
DR Pfam: PF00667; FAD_binding; 1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
SQ SEQUENCE 1205 AA; 133045 MW; C150CDEB01685BA5 CRC64;

Query Match 68.9%; Score 71; DB 6; Length 1205;
Best Local Similarity 80.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIVPFRFQWQRLHD 15
   || ||| ||| |||
DB 1019 GIAPFRGFWQGRLLD 1033

RESULT 12
ID 077104 PRELIMINARY: PRT; 1206 AA.
AC 077104;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE NITRIC OXIDE SYNTHASE.
OS NOS.
GN Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC SpHINGIOidea; SpHINGidae; SpHINGinae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98409773; PubMed=9736646;
RA Nighorn A., Gibson N.J., Rivers D.M., Hildebrand J.G., Morton D.B.;
RT "The nitric oxide-cGMP pathway may mediate communication between
RT sensory afferents and projection neurons in the antennal lobe of
RT Manduca sexta.";
RL J. Neurosci. 18:7244-7255(1998).
DR EMBL; AF062749; AAC61262.1; -.
DR HSSP; P29477; 1DD7.
DR InterPro: IPR001094; -.
DR InterPro: IPR001433; -.
DR InterPro: IPR003097; -.
DR Pfam: PF00175; oxidored_fad; 1.
DR Pfam: PF00667; FAD_binding; 1.
DR PRINTS: PR00369; FLAVODOXIN.
SQ SEQUENCE 1206 AA; 137032 MW; BF5528FC99ADECE6 CRC64;

Query Match 54.4%; Score 56; DB 5; Length 1206;
Best Local Similarity 44.4%; Pred. No. 0.54;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GIVPFRFQWQRLHDSQH 18
   |: ||| || | | :
DB 1033 GVAPFRGFWHRRHQMN 1050

RESULT 13
Q9VKP8 PRELIMINARY: PRT; 1349 AA.
AC Q9VKP8; Q90096;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2001 (TREMBLrel. 16, Last annotation update)
DE NITRIC OXIDE SYNTHASE (EC 1.14.13.39) (DNOS).
GN NOS OR CG6713.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

```

[1]

RN

SEQUENCE FROM N.A.

RP

STRAIN=BERKELEY;

RX

MEDLINE=20196006; PubMed=10731132;

RA

Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Durlin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Spier E., Spidling A.C., Stapleton M., Strong R., Sun E.,

Swigkes R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,

Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000).

[2]

RN

SEQUENCE FROM N.A.

RP

Stasiv Y., Regulski M., Tully T., Enikolopov G.;

"Structural organization and alternative splicing of the Drosophila

nitric oxide synthase gene.";

RT

Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RL

FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE

CC

WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.

CC

-!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +

NITRIC OXIDE + N NADP(+).

CC

-!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN (BY

SIMILARITY).

CC

-!- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN.

CC

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM/DNOS-1 (SHOWN HERE)

AND A SHORT FORM/DNOS-2; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC

-!- SIMILARITY: BELONGS TO THE NOS FAMILY.

CC

EMBL; AE003630; AAF53014.1; -.

DR

EMBL; AF215700; AAF25682.1; -.

DR

EMBL; AF215691; AAF25682.1; JOINED.

DR

EMBL; AF215692; AAF25682.1; JOINED.

DR

EMBL; AF215693; AAF25682.1; JOINED.

DR

EMBL; AF215694; AAF25682.1; JOINED.

DR

EMBL; AF215695; AAF25682.1; JOINED.

DR

EMBL; AF215696; AAF25682.1; JOINED.

DR

EMBL; AF215697; AAF25682.1; JOINED.

DR

EMBL; AF215698; AAF25682.1; JOINED.

DR

EMBL; AF215699; AAF25682.1; JOINED.

DR

HSSP; P29477; 1DD7.

DR

FlyBase: FBgn0011676; Nos.

DR

InterPro: IPR001094; -.

DR

InterPro: IPR001433; -.

DR

```

DR InterPro: IPR001709; -.
DR InterPro: IPR001993; -.
DR InterPro: IPR003097; -.
DR Pfam: PF00175; oxidored_fad; 1.
DR Pfam: PF00667; FAD_binding; 1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_1.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
FT CONFLICT 373 373 T -> S (IN REF. 2).
FT CONFLICT 1197 1197 S -> R (IN REF. 2).
SQ SEQUENCE 1349 AA; 151713 MW; E19D8CBAEFAF76FC CRC64;

Query Match 54.4%; Score 56; DB 5; Length 1349;
Best Local Similarity 81.8%; Pred. No. 0.6;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIVPFRSFQQ 11
Db 1182 GIAPFRSFQQE 1192

RESULT 14
Q42697 PRELIMINARY; PRT; 255 AA.
AC Q42697;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE FERREDOXIN NADP REDUCTASE (EC 1.18.1.2) (FERREDOXIN-NADP(+))
DE REDUCTASE (ADRENODOXIN REDUCTASE) (FRAGMENT).
GN PETH.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=137C;
RX MEDLINE=95142635; PubMed=7840625;
RA Decottignies P., Le Marechal P., Jacquot J.P., Schmitter J.M.,
RA Gadai P.;
RT "Primary structure and post-translational modification of ferredoxin-
RT NADP reductase from Chlamydomonas reinhardtii.";
RL Arch. Biochem. Biophys. 316:249-259(1995).
CC -|- CATALYTIC ACTIVITY: REDUCED FERREDOXIN + NADP(+) = OXIDIZED
CC FERREDOXIN + NADPH.
CC -|- COFACTOR: FAD.
DR EMBL: X78851; CAA55406.1; -.
DR HSP: P00455; 1FNC.
DR Mendel; 7667; Chlre; PETH; 7667.
DR InterPro: IPR001433; -.
DR InterPro: IPR001709; -.
DR Pfam: PF00175; oxidored_fad; 1.
DR PRINTS: PR00371; FPNCR.
KW Oxidoreductase.
FT NON_TER 1 1
FT NON_TER 255 255
SQ SEQUENCE 255 AA; 28594 MW; 628CFED2592A1999 CRC64;

```

```

Query Match 49.5%; Score 51; DB 10; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.75;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIVPFRSFQQ 11
Db 115 GIAPFRSFWR 125

RESULT 15

```

```

Q9S9E0
ID Q9S9E0 PRELIMINARY; PRT; 320 AA.
AC Q9S9E0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE FERREDOXIN-NADP REDUCTASE (EC 1.18.1.2).
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE.
RX MEDLINE=95142635; PubMed=7840625;
RA Decottignies P., Le Marechal P., Jacquot J.P., Schmitter J.M.,
RA Gadai P.;
RT "Primary structure and post-translational modification of ferredoxin-
RT NADP reductase from Chlamydomonas reinhardtii.";
RL Arch. Biochem. Biophys. 316:249-259(1995).
DR HSP: P00455; 1FNC.
DR InterPro: IPR001433; -.
DR InterPro: IPR001709; -.
DR Pfam: PF00175; oxidored_fad; 1.
DR PRINTS: PR00371; FPNCR.
SQ SEQUENCE 320 AA; 35571 MW; DB7897520C5B87E7 CRC64;

Query Match 49.5%; Score 51; DB 10; Length 320;
Best Local Similarity 72.7%; Pred. No. 0.95;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIVPFRSFQQ 11
Db 180 GIAPFRSFWR 190

```

Search completed: September 10, 2001, 14:11:11  
Job time: 590 sec

Result No.	Score	Query		ID	Description
		Match	Length		
1	99	96.1	496	1 NOS2_RABIT	O19114 oryctolagus
2	99	96.1	1144	1 NOS2_MOUSE	P29477 mus musculus
3	99	96.1	1147	1 NOS2_RAT	P06518 rattus norv
4	99	96.1	1153	1 NS2A_HUMAN	P05228 homo sapien
5	91	88.3	1147	1 NS2D_HUMAN	O60591 homo sapien
6	86	83.5	69	1 NS2C_HUMAN	Q14961 homo sapien
7	84	81.6	1149	1 NOS2_CAVPO	O54705 cavia porce
8	79	76.7	246	1 NOS2_BOVIN	Q27995 bos taurus
9	78	75.7	1429	1 NOS1_MOUSE	Q92014 mus musculus
10	78	75.7	1429	1 NOS1_RAT	P29476 rattus norv
11	78	75.7	1434	1 NOS1_HUMAN	P29475 homo sapien
12	76	73.8	1136	1 NOS2_CHICK	Q90703 gallus gall
13	75	72.8	1202	1 NOS3_HUMAN	P29474 homo sapien
14	75	72.8	1204	1 NOS3_BOVIN	P29473 bos taurus
15	75	72.8	1204	1 NOS3_PIG	Q82969 sus scrofa
16	73	70.9	919	1 NOS3_RAT	Q62600 rattus norv
17	73	70.9	1201	1 NOS3_MOUSE	P70313 mus musculus
18	69	67.0	1153	1 NOS1LYST	O61309 lymnaea sta
19	68	66.0	1435	1 NOS1_RABIT	O19132 oryctolagus
20	59	57.3	1174	1 NOS_RHOPR	Q62640 rhodnius pr
21	57	55.3	1247	1 NOS_ANOST	O61608 anopheles s
22	56	54.4	1350	1 NOS_DROME	Q27571 drosophila
23	53	51.5	601	1 CYSJ_BUCAI	P57503 buchera ap
24	52	50.5	598	1 CYSJ_ECOLI	P38038 escherichia
25	52	50.5	598	1 CYSJ_SALTY	P38039 salmonella
26	51	49.5	354	1 FENR_CHLRE	P53991 chlamydomon
27	47	45.6	364	1 ERG3_CANGA	P50860 candida gla
28	46	44.7	714	1 NCPR_CATRO	O50001 catharanthu
29	46	44.7	872	1 MGR2_RAT	P31421 rattus norv
30	45	43.7	79	1 NS2B_HUMAN	P81272 homo sapien
31	45	43.7	571	1 YB63_SCHPO	Q09744 schizosacch
32	44	42.7	407	1 YD6D_SCHPO	Q10325 schizosacch
33	44	42.7	522	1 CYSJ_THIRO	P52674 thiocapsa r



DR PDB: 1DWX; 06-FEB-00.  
DR PDB: 1QOM; 15-DEC-99.  
DR PDB: 1DD7; 29-MAR-00.  
DR MGD: MGI:97361; Nos2.  
DR InterPro: IPR001094; -  
DR InterPro: IPR001433; -  
DR InterPro: IPR001709; -  
DR InterPro: IPR003097; -  
DR Pfam: PF00667; FAD\_binding; 1.  
DR Pfam: PF00175; oxidored\_fad; 1.  
DR PRINTS: PR00369; FLAVODOXIN.  
DR PRINTS: PR00371; FPNCR.  
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;  
KW Zinc; Metal-binding; Multigene family; 3D-structure.  
FT BINDING 194 194  
FT DOMAIN 503 523  
FT NP\_BIND 617 648  
FT NP\_BIND 761 772  
FT NP\_BIND 897 907  
FT NP\_BIND 972 990  
FT NP\_BIND 1070 1085  
FT METAL 104 104  
FT METAL 109 109  
FT VARIANT 211 211  
FT VARIANT 967 967  
FT VARIANT 968 968  
FT CONFLICT 19 19  
FT CONFLICT 191 191  
FT CONFLICT 844 844  
SQ SEQUENCE 1144 AA; 130574 MW; 0735BE676113457F CRC64;  
Query Match 96.1%; Score 99; DB 1; Length 1144;  
Best Local Similarity 94.4%; Pred. No. 8.9e-09;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 GIVPFRFWQRLHDSQH 18  
II |||||  
DB 979 GIAPFRFWQRLHDSQH 996  
RESULT 3  
ID NOS2\_RAT STANDARD; PRT; 1147 AA.  
AC Q06518; P97774; Q35765; Q35766; Q64558; Q64005; Q63267;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)  
DE (INDUCIBLE NOS) (INOS).  
GN NOS2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBTaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Vascular smooth muscle;  
RX MEDLINE=93191721; PubMed=7680561;  
RA Nunokawa Y., Ishida N., Tanaka S.;  
RT "Cloning of inducible nitric oxide synthase in rat vascular smooth  
RT muscle cells.";  
RL Biochem. Biophys. Res. Commun. 191:89-94(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Wistar; TISSUE=pancreatic islets;  
RX MEDLINE=93309542; PubMed=7540573;  
RA Karlisen A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J.,  
RA Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,  
RA Mandrup-Poulsen T., Boel E., Nerup J.;  
RT "Cloning and expression of cytokine-inducible nitric oxide synthase  
RT cDNA from rat islets of Langerhans.";  
RL Diabetes 44:753-758(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Astrocytes;  
RX MEDLINE=94231594; PubMed=7513765;  
RA Galea E., Reis D.J., Feinstein D.L.;  
RT "Cloning and expression of inducible nitric oxide synthase from rat  
RT astrocytes.";  
RL J. Neurosci. Res. 37:406-414(1994).  
RN [4]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=94039059; PubMed=7693462;  
RA Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K.,  
RA Kawasaki H., Sugimura T., Esumi H.;  
RT "Molecular cloning of a cDNA encoding an inducible  
RT calmodulin-dependent nitric-oxide synthase from rat liver and its  
RT expression in COS 1 cells.";  
RL Eur. J. Biochem. 217:37-43(1993).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Hepatocytes;  
RX MEDLINE=93221515; PubMed=7682072;  
RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;  
RT "Hepatocytes and macrophages express an identical cytokine inducible  
RT nitric oxide synthase gene.";  
RL Biochem. Biophys. Res. Commun. 191:767-774(1993).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Aorta;  
RX MEDLINE=94325351; PubMed=7519448;  
RA Geng Y.J., Almquist M., Hansson G.K.;  
RT "cDNA cloning and expression of inducible nitric oxide synthase from  
RT rat vascular smooth muscle cells.";  
RL Biochim. Biophys. Acta 1218:421-424(1994).  
RN [7]  
RP SEQUENCE FROM N.A.  
RA Kosuga K., Yui Y., Hattori R., Sase K., Eizawa H., Aoyama T.,  
RA Inoue R., Sasayama S.;  
RT "Cloning of an inducible nitric oxide synthase from rat  
RT polymorphonuclear neutrophils.";  
RL Endothelium 2:217-221(1994).  
RN [8]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97070590; PubMed=8913516;  
RA Tsutsumishita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,  
RA Futaki S., Niwa M.;  
RT "Sequence analysis of inducible nitric oxide synthase in rat kidney,  
RT lung, and uterus.";  
RL Biol. Pharm. Bull. 19:1374-1376(1996).  
RN [9]  
RP SEQUENCE OF 426-788 FROM N.A.  
RC STRAIN=DAHL/RAPP SALT SENSITIVE STRAIN; TISSUE=Vascular smooth muscle;  
RX MEDLINE=98195092; PubMed=9535415;  
RA Chen P.Y., Gladish R.D., Sanders P.W.;  
RT "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp  
RT salt-sensitive rats.";  
RL Hypertension 31:918-924(1998).  
RN [10]  
RP SEQUENCE OF 509-740 FROM N.A.  
RC STRAIN=WISTAR; TISSUE=Renal glomerulus;  
RA Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;  
RT "Advances in the studies of NO synthesis regulation in mesangial  
RT cells.";  
RL Nephrologia 16:35-39(1996).  
RN [11]  
RP SEQUENCE OF 479-655 FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Renal glomerulus;  
RX MEDLINE=94276509; PubMed=7516453;  
RA Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montani D.,  
RA Klahr S.;  
RT "Location of an inducible nitric oxide synthase mRNA in the normal  
RT kidney.";  
RL Kidney Int. 45:998-1005(1994).

[12]  
 RN SEQUENCE OF 420-479 FROM N.A.  
 RP TISSUE=Myocardium;  
 RA Michel T., Balligand J.-L.;  
 RT "Isolation and characterization of INOS from rat cardiocytes."; 1994;  
 Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
 RL -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.  
 CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) -> CITRULLINE +  
 NITRIC OXIDE + N NADP(+).  
 CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 THE ENZYME.  
 CC -!- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN  
 INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE  
 EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL  
 CC MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY  
 SIMILARITY).  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- TISSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY IN THE  
 MEDULLARY THICK ASCENDING LIMB, WITH MINOR AMOUNTS IN THE  
 CC MEDULLARY COLLECTING DUCT AND VASA RECTA BUNDLE.  
 CC -!- INDUCTION: BY INTERFERON GAMMA AND LIPOPOLYSACCHARIDE.  
 CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 -----  
 DR EMBL; D14051; BAA03138.1; -;  
 DR EMBL; U26686; AAB85861.1; -;  
 DR EMBL; U03899; AAC13747.1; -;  
 DR EMBL; D12520; BAA02090.1; -;  
 DR EMBL; L12562; AAA41720.1; -;  
 DR EMBL; X76881; CAA54208.1; -;  
 DR EMBL; D4591; BAA07994.1; -;  
 DR EMBL; D3661; BAA12035.1; -;  
 DR EMBL; AF006619; AAC16401.1; -;  
 DR EMBL; AF006620; AAC16402.1; -;  
 DR EMBL; U48829; AAB18620.1; -;  
 DR EMBL; S71597; AAB31028.2; -;  
 DR EMBL; L36063; AAC02242.1; -;  
 DR PIR; JC1472; JC1472; -;  
 DR HSP; P29477; INOC; -;  
 DR InterPro; IPR001094; -;  
 DR InterPro; IPR001433; -;  
 DR InterPro; IPR001709; -;  
 DR InterPro; IPR003097; -;  
 DR Pfam; PF00667; FAD\_binding; 1;  
 DR Pfam; PF00175; oxidored\_fad; 1;  
 DR PRINTS; PR00369; FLAVODOXIN;  
 DR PRINTS; PR00371; FPNCR;  
 KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;  
 Zinc; Metal-binding; Multigene family;  
 FT BINDING 197 197  
 FT DOMAIN 506 526  
 FT NP\_BIND 520 551  
 FT NP\_BIND 764 775  
 FT NP\_BIND 900 910  
 FT NP\_BIND 975 993  
 FT NP\_BIND 1073 1088  
 FT METAL 107 107  
 FT METAL 112 112  
 FT CONFLICT 10 10  
 FT CONFLICT 72 72  
 FT CONFLICT 107 107  
 FT CONFLICT 128 128  
 FT CONFLICT 130 130  
 FT CONFLICT 171 171  
 E -> G (IN REF. 8).  
 R -> K (IN REF. 7).  
 H -> Y (IN REF. 1).  
 C -> R (IN REF. 3).  
 D -> V (IN REF. 8).  
 P -> H (IN REF. 3).  
 E -> G (IN REF. 8).

FT CONFLICT 195 195  
 FT CONFLICT 248 248  
 FT CONFLICT 264 264  
 FT CONFLICT 277 277  
 FT CONFLICT 348 348  
 FT CONFLICT 349 349  
 FT CONFLICT 380 380  
 FT CONFLICT 395 395  
 FT CONFLICT 412 412  
 FT CONFLICT 477 477  
 FT CONFLICT 513 513  
 FT CONFLICT 515 515  
 FT CONFLICT 545 545  
 FT CONFLICT 551 551  
 FT CONFLICT 556 556  
 FT CONFLICT 564 564  
 FT CONFLICT 570 570  
 FT CONFLICT 583 583  
 FT CONFLICT 591 591  
 FT CONFLICT 591 591  
 FT CONFLICT 619 619  
 FT CONFLICT 664 664  
 FT CONFLICT 679 679  
 FT CONFLICT 690 690  
 P -> S (IN REF. 8).  
 S -> T (IN REF. 3 AND 5).  
 Y -> I (IN REF. 3).  
 D -> E (IN REF. 3).  
 A -> P (IN REF. 1).  
 V -> A (IN REF. 6).  
 F -> L (IN REF. 2, 7 AND 8).  
 R -> S (IN REF. 4).  
 V -> A (IN REF. 3).  
 M -> I (IN REF. 12).  
 T -> R (IN REF. 10).  
 L -> W (IN REF. 11).  
 G -> R (IN REF. 11).  
 A -> R (IN REF. 10).  
 A -> S (IN REF. 11).  
 T -> N (IN REF. 11).  
 E -> D (IN REF. 11).  
 L -> P (IN REF. 5 AND 9).  
 G -> A (IN REF. 11).  
 G -> V (IN REF. 1 AND 6).  
 A -> R (IN REF. 2).  
 D -> G (IN REF. 10).  
 ET -> VP (IN REF. 1).  
 Q -> P (IN REF. 10).  
 Query Match 96.1%; Score 99; DB 1; Length 1147;  
 Best Local Similarity 94.4%; Pred. No. 9e-09;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GIVPFRSFQQRRLHDSQH 18  
 DB 982 GIAPFRSFQQRRLHDSQH 999  
 RESULT 4  
 ID NS2A\_HUMAN STANDARD; PRT; 1153 AA.  
 AC P35228; Q16692; O60757; Q16263;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)  
 DE (INDUCIBLE NOS) (INOS) (HEPATOCYTE NOS) (HEP-NOS).  
 GN NOS2A OR NOS2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93234523; PubMed=7682706;  
 RA Geller D.A., Lowenstein C.J., Shapiro R.A., Nussler A.K.,  
 RA di Silvio M., Wang S.C., Nakayama D.K., Simmons R.L., Snyder S.H.,  
 RA Billiar T.R.;  
 RT "Molecular cloning and expression of inducible nitric oxide synthase  
 from human hepatocytes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:3491-3495(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colorectal adenocarcinoma;  
 RX MEDLINE=94032282; PubMed=7692964;  
 RA Sherman P.A., Laubach V.E., Reep B.R., Wood E.R.;  
 RT "Purification and cDNA sequence of an inducible nitric oxide synthase  
 from a human tumor cell line.";  
 RL Biochemistry 32:11600-11605(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Chondrocytes;  
 RX MEDLINE=94068614; PubMed=7504305;  
 RA Charles I.G., Palmer R.M.J., Hickery M.S., Bayliss M.T.,  
 RA Chubb A.P., Hall V.S., Moss D.W., Moncada S.;  
 RT "Cloning, characterization, and expression of a cDNA encoding an

RT inducible nitric oxide synthase from the human chondrocyte.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:11419-11423(1993).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Articular chondrocytes;  
 RX MEDLINE-94368816; PubMed-7522054;  
 RA Maier R., Bilbe G., Rediske J., Lotz M.;  
 RT "Inducible nitric oxide synthase from human articular chondrocytes:  
 RL cDNA cloning and analysis of mRNA expression.";  
 RN Biochim. Biophys. Acta 1208:145-150(1994).  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Retina;  
 RX MEDLINE-95091827; PubMed-7528017;  
 RA Park C.-S., Pardhasaradhi K., Gianotti C., Villegas E., Krishna G.;  
 RT "Human retina expresses both constitutive and inducible isoforms of  
 RL nitric oxide synthase mRNA.";  
 RN Biochem. Biophys. Res. Commun. 205:85-91(1994).  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Glioblastoma;  
 RX MEDLINE-95155267; PubMed-7531687;  
 RA Hokari A., Zeniya M., Esumi H.;  
 RT "Cloning and functional expression of human inducible nitric oxide  
 RL synthase (NOS) cDNA from a glioblastoma cell line A-172.";  
 RN J. Biochem. 116:575-581(1994).  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Airway epithelium;  
 RX MEDLINE-95372368; PubMed-7544004;  
 RA Guo F.H., de Raevae R.H., Rice T.W., Stuehr D.J., Thunnissen F.B.J.M.,  
 RL Brzurum S.C.;  
 RT "Continuous nitric oxide synthesis by inducible nitric oxide synthase  
 RL in normal human airway epithelium in vivo.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 92:7809-7813(1995).  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Cardiac myocytes;  
 RX MEDLINE-97304504; PubMed-9160867;  
 RA Luss H., Li R.-K., Shapiro R.A., Tzeng E., McGowan F.X., Yoneyama T.,  
 RL Hatakeyama K., Geller D.A., Mickle D.A.G., Simmons R.L.,  
 RA Billiar T.R.;  
 RT "Differentiated human ventricular cardiac myocytes express  
 RL inducible nitric oxide synthase mRNA but not protein in response to  
 RL IL-1, TNF, IFN-gamma, and LPS.";  
 RN J. Mol. Cell. Cardiol. 29:1153-1165(1997).  
 RP SEQUENCE OF 380-473 FROM N.A.  
 RC TISSUE-Kidney;  
 RX MEDLINE-95165725; PubMed-7532248;  
 RA McLeay J.S., Chatterjee P., Nicolson A.G., Jardine A.G., McKay N.G.,  
 RL Ralston S.H., Grabowski P., Hailes N.E., Macleod A.M.,  
 RA Hawksworth G.M.;  
 RT "Nitric oxide production by human proximal tubular cells: a novel  
 RL immunomodulatory mechanism?";  
 RN Kidney Int. 46:1043-1049(1994).  
 RP CHARACTERIZATION.  
 RX MEDLINE-96047340; PubMed-7558036;  
 RA Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G.,  
 RA Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;  
 RT "Three members of the nitric oxide synthase II gene family (NOS2A,  
 RL NOS2B, and NOS2C) colocalize to human chromosome 17.";  
 RN Genomics 27:526-530(1995).  
 RP CHARACTERIZATION.  
 RX MEDLINE-98389865; PubMed-9721329;  
 RA Taylor B.S., Alarcon L.H., Billiar T.R.;  
 RT "Inducible nitric oxide synthase in the liver: regulation and  
 RL function.";  
 RN Biochimica 63:766-781(1998).  
 RL [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 74-504.

RX MEDLINE-99340067; PubMed-10409685;  
 RA Li H., Raman C.S., Glaser C.B., Blasko E., Young T.A., Parkinson J.F.,  
 RA Whitlow M., Poulos T.L.;  
 RT "Crystal structures of zinc-free and -bound heme domain of human  
 RT inducible nitric-oxide synthase. Implications for dimer stability and  
 RT comparison with endothelial nitric-oxide synthase.";  
 RL J. Biol. Chem. 274:21276-21284(1999).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 82-528.  
 RX MEDLINE-99173237; PubMed-10074942;  
 RA Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,  
 RA Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,  
 RA Weber P.C.;  
 RT "Structural characterization of nitric oxide synthase isoforms  
 RT reveals striking active-site conservation.";  
 RL Nat. Struct. Biol. 6:233-242(1999).  
 CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO  
 CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.  
 CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +  
 CC NITRIC OXIDE + N NADP(+).  
 CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 CC THE ENZYME (BY SIMILARITY).  
 CC -!- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST  
 CC WITH MOUSE NOS2). ASPIRIN INHIBITS EXPRESSION AND FUNCTION OF THIS  
 CC ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF  
 CC TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE  
 CC CATALYTIC ACTIVITY (BY SIMILARITY).  
 CC -!- SUBUNIT: HOMODIMER.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE LIVER, RETINA, BONE CELLS AND  
 CC AIRWAY EPITHELIAL CELLS OF THE LUNG. NOT EXPRESSED IN THE  
 CC PLATELETS.  
 CC -!- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES.  
 CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; L09210; AAA59171.1; -;  
 DR EMBL; L24553; AAA36375.1; -;  
 DR EMBL; X73029; CAA51512.1; -;  
 DR EMBL; U05810; AAA56666.1; -;  
 DR EMBL; U31511; AAB49041.1; -;  
 DR EMBL; D26525; BAA05531.1; -;  
 DR EMBL; U20141; AAB60366.1; -;  
 DR EMBL; AF068236; AAC19133.1; -;  
 DR EMBL; S75615; AAD14179.1; -;  
 DR PIR; A47475; A47475.  
 DR PDB; 1NSI; 07-JAN-00.  
 DR PDB; 2NSI; 07-JAN-00.  
 DR PDB; 4NOS; 04-FEB-00.  
 DR MIM; I63730; -;  
 DR InterPro; IPR001094; -;  
 DR InterPro; IPR001433; -;  
 DR InterPro; IPR001709; -;  
 DR InterPro; IPR003097; -;  
 DR Pfam; PF00667; FAD-binding; 1.  
 DR Pfam; PF00175; oxidoreductase; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 KW Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;  
 KW Heme; Phosphorylation; Zinc; Metal-binding; Multigene family;  
 KW 3D-structure.  
 FT BINDING 200 200 HEME.  
 FT DOMAIN 509 529 CALMODULIN-BINDING (POTENTIAL).  
 FT NP\_BIND 623 654 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FT NP\_BIND 767 778 FAD (ADP PART) (BY SIMILARITY).  
 FT

```
FT NP_BIND 903 913 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 978 996 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 1076 1091 NADP (ADP PART) (BY SIMILARITY).
FT METAL 110 110 ZINC.
FT METAL 115 115 ZINC.
FT MOD_RES 234 234 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 578 578 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 892 892 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT CONFLICT 23 23 D -> G (IN REF. 4).
FT CONFLICT 154 154 F -> L (IN REF. 4).
FT CONFLICT 177 177 G -> V (IN REF. 4).
FT CONFLICT 266 266 R -> H (IN REF. 8).
FT CONFLICT 423 423 L -> I (IN REF. 2).
FT CONFLICT 439 439 A -> T (IN REF. 8).
FT CONFLICT 608 608 S -> L (IN REF. 5 AND 6).
FT CONFLICT 676 676 T -> I (IN REF. 7).
FT CONFLICT 800 800 T -> A (IN REF. 4).

Query Match 96.1%; Score 99; DB 1; Length 1153;
Best Local Similarity 94.4%; Pred. No. 9e-09;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIVPFRSFQQRRLHDSQ 18
Db 985 GIAPRSFQQRRLHDSQ 1002

RESULT 5
NS2D_HUMAN STANDARD; PRT; 1147 AA.
ID NS2D_HUMAN STANDARD; PRT; 69 AA.
AC Q14961;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE NITRIC OXIDE SYNTHASE, INDUCIBLE IID (EC 1.14.13.39) (NOS, TYPE II D)
DE (INDUCIBLE NOS) (INOS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle, and Heart muscle;
RX MEDLINE=99066690; PubMed=9851365;
RA Adams V., Krabbes S., Jiang H., Yu J., Rahmel A., Gielen S.,
RA Schuler G., Hambrecht R.;
RT "Complete coding sequence of inducible nitric oxide synthase from
RT human heart and skeletal muscle of patients with chronic heart
RT failure.";
RL Nitric Oxide 2:242-249(1998).
CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO
CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS. MAY BE INVOLVED IN
CC THE PATHOGENESIS OF DILATED CARDIOMYOPATHY OR OF EXERCISE
CC INTOLERANCE OBSERVED IN PATIENTS WITH CHRONIC HEART FAILURE.
CC -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +
CC NITRIC OXIDE + N NADP(+).
CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME (BY SIMILARITY).
CC -1- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (BY
CC SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE HEART AND SKELETAL MUSCLE
CC DURING CHRONIC HEART FAILURE, BUT NOT IN HEALTHY INDIVIDUALS.
CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
```

```
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF049656; AAC83553.1; -
CC EMBL; AF051164; AAC83554.1; -
CC HSSP; P29477; INOC.
CC InterPro; IPR001094; -
CC InterPro; IPR001433; -
CC InterPro; IPR001709; -
CC InterPro; IPR003097; -
CC Pfam; PF00667; FAD_binding_1;
CC Pfam; PF00175; oxigored_fad; 1.
CC PRINTS; PR00369; FLAVODOXIN.
CC PRINTS; PR00371; FPNCR.
CC Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;
CC Heme; Zinc; Metal-binding; Multigene family.
CC BINDING 197 197 HEME (BY SIMILARITY).
CC DOMAIN 506 526 FMN (PYRIMIDINE PART) (BY SIMILARITY).
CC NP_BIND 620 651 FAD (ADP PART) (BY SIMILARITY).
CC NP_BIND 764 775 FAD (FLAVIN PART) (BY SIMILARITY).
CC NP_BIND 900 910 NADP (RIBOSE PART) (BY SIMILARITY).
CC NP_BIND 975 993 NADP (ADP PART) (BY SIMILARITY).
CC NP_BIND 1073 1088 ZINC (BY SIMILARITY).
CC METAL 107 107 ZINC (BY SIMILARITY).
CC METAL 112 112 ZINC (BY SIMILARITY).
CC CONFLICT 248 248 N -> S (IN AAC83554).
CC CONFLICT 271 271 D -> A (IN AAC83554).
CC CONFLICT 399 399 G -> E (IN AAC83554).
CC CONFLICT 640 640 P -> Q (IN AAC83554).
CC CONFLICT 731 731 A -> T (IN AAC83554).
CC CONFLICT 937 937 H -> N (IN AAC83554).
CC CONFLICT 1008 1009 TL -> NF (IN AAC83554).
CC CONFLICT 1024 1024 E -> K (IN AAC83554).
CC CONFLICT 1076 1076 I -> L (IN AAC83554).
CC CONFLICT 1129 1129 F -> V (IN AAC83554).
CC SEQUENCE 1147 AA; 130528 MW; FF7E4C7ABA76D820 CRC64;

Query Match 88.3%; Score 91; DB 1; Length 1147;
Best Local Similarity 94.1%; Pred. No. 2e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIVPFRSFQQRRLHDSQ 17
Db 982 GIAPRSFQQRRLHDSQ 998

RESULT 6
NS2C_HUMAN STANDARD; PRT; 69 AA.
ID NS2C_HUMAN STANDARD; PRT; 69 AA.
AC Q14961;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NITRIC-OXIDE SYNTHASE IIC (EC 1.14.13.39) (NOS, TYPE II C) (NOSIIC)
DE (FRAGMENT).
GN NOS2C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=96047340; PubMed=7558036;
RA Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G.,
RA Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;
RT "Three members of the nitric oxide synthase II gene family (NOS2A,
RT NOS2B, and NOS2C) colocalize to human chromosome 17.";
RL Genomics 27:526-530(1995).
CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO
CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.
CC -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +
```



CC NITRIC OXIDE + N NADP(+).

CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES

CC TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF

CC THE ENZYME (BY SIMILARITY).

CC -!- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (BY

CC SIMILARITY).

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- SUBUNIT: BELONGS TO THE NOS FAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL: U18335; AAC50245.1; -.

DR EMBL: U18334; AAC50245.1; JOINED.

DR HSSP: P00388; IAWO.

DR MIM: 600720; -.

DR OXidoreductase: NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;

KW Heme; Multigene family.

FT NON\_TER 1 25 NADP (RIBOSE PART) (BY SIMILARITY).

FT NP\_BIND 7 69

FT NON\_BIND 69 69

FT SEQUENCE 69 AA; 8432 MW; 2C29D595F93FB293 CRC64;

Query Match 83.5%; Score 86; DB 1; Length 69;

Best Local Similarity 88.2%; Pred. No. 6.3e-08;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIVPFRSFQWQRLHDSQ 17

DB 14 GIAPFHSFQWQRLHDSQ 30

RESULT 7

ID NOS2\_CAVPO STANDARD; PRT; 1149 AA.

AC O54705;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)

DE (INDUCIBLE NOS) (INOS).

GN NOS2 OR NOS.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

OX NCBI\_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HARTLEY; TISSUE=Lung;

RX MEDLINE=98343971; PubMed=9677342;

RA Shirato M., Sakamoto T., Uchida Y., Nomura A., Ishii Y., Iijima H.,

RA Goto Y., Hasegawa S.;

RT "Molecular cloning and characterization of Ca2+-dependent inducible

RT nitric oxide synthase from guinea-pig lung.";

RL Biochem. J. 333:795-799(1998).

CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE

CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.

CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +

CC NITRIC OXIDE + N NADP(+).

CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES

CC TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF

CC THE ENZYME (BY SIMILARITY).

CC -!- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST

CC WITH MOUSE NOS2).

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE LUNG AND COLON. NOT DETECTED

CC IN THE HEART, AORTA, LIVER, KIDNEY, AND SPLEEN.

CC -!- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS) IN KIDNEY, SPLEEN, AND

CC COLON. EXPRESSION IS REDUCED IN THE PRESENCE OF LPS IN LUNG.

CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL: AF027180; AAC33177.1; -.

DR HSSP: P29477; 2NOS.

DR InterPro: IPR001094; -.

DR InterPro: IPR001433; -.

DR InterPro: IPR001709; -.

DR InterPro: IPR003097; -.

DR Pfam: PF00667; FAD\_binding; 1.

DR Pfam: PF00175; Oxidoreductase; 1.

DR PRINTS: PR00369; FLAVODOXIN.

DR PRINTS: PR00371; FPNCR.

KW Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;

KW Heme; Multigene family.

FT BINDING 199 199

FT DOMAIN 508 528

FT NP\_BIND 622 653

FT NP\_BIND 766 777

FT NP\_BIND 902 912

FT NP\_BIND 977 995

FT NP\_BIND 1075 1090

FT SEQUENCE 1149 AA; 130631 MW; 66D595A2486DB50E CRC64;

Query Match 81.6%; Score 84; DB 1; Length 1149;

Best Local Similarity 77.8%; Pred. No. 3e-06;

Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIVPFRSFQWQRLHDSQ 18

DB 984 GIAPFHSFQWQRLHDSQ 1001

RESULT 8

ID NOS2\_BOVIN STANDARD; PRT; 246 AA.

AC Q27995; Q27985;

DT 01-NOV-1997 (Rel. 35, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)

DE (INDUCIBLE NOS) (INOS) (NOSII) (FRAGMENTS).

GN NOS2.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE OF 1-110 FROM N.A.

RC TISSUE=Bone marrow macrophage;

RX MEDLINE=95238970; PubMed=7536776;

RA Adler H., Frech B., Thoeny M., Pfister H., Peterhans E., Jung T.W.;

RT "Inducible nitric oxide synthase in cattle. Differential cytokine

RT regulation of nitric oxide synthase in bovine and murine

RT macrophages.";

RL J. Immunol. 154:4710-4718(1995).

RN [2]

RP SEQUENCE OF 111-246 FROM N.A.

RC TISSUE=Pulmonary artery;

RX MEDLINE=96047340; PubMed=7558036;

RA Bloch K.D., Wolfgram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G.,

RA Lepore J.J., Filippov G., Jacob H.J., Bloch D.B.;

RT "Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, and NOS2C) colocalize to human chromosome 17.";  
 RL Genomics 27:526-530(1995).  
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO  
 CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.  
 CC -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) -> CITRULLINE +  
 CC NITRIC OXIDE + N NADP(+).  
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 CC TETRAHYDROBIPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 CC THE ENZYME (BY SIMILARITY).  
 CC -1- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY  
 CC SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U14640; AAC48470.1; -;  
 CC EMBL; U18331; AAC48479.1; -;  
 CC HSSP; P29477; 3NOD.  
 CC InterPro: IPR001433; -;  
 CC Pfam; PF00175; oxidored\_fad; 1.  
 CC Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;  
 CC Multigene family.  
 CC NON\_TER 1 1  
 CC BINDING 35 35 HEME (BY SIMILARITY).  
 CC NP\_BIND 200 215 NADP (ADP PART) (BY SIMILARITY).  
 CC NON\_CONS 110 111  
 CC NON\_TER 246 246  
 CC SEQUENCE 246 AA; 28748 MW; 87C2E330C86A27E4 CRC64;  
 SQ  
 Query Match 76.7%; Score 79; DB 1; Length 246;  
 Best Local Similarity 80.0%; Pred. No. 3.8e-06;  
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4 PFRSFQWQRLHDSOH 18  
 |||||  
 Db 112 PFRSFQWQRLHDSOH 126  
 RESULT 9  
 ID NOS1\_MOUSE STANDARD; PRT; 1429 AA.  
 AC Q920J4; 064208;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL  
 DE NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS).  
 GN NOS1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS N-NOS-1 AND N-NOS-2).  
 RC STRAIN=BA1B/C; TISSUE=Brain;  
 RX MEDLINE=93312283; PubMed=7686743;  
 RA Ogura T., Yokoyama T., Fujisawa H., Kurashima Y., Esumi H.;  
 RT "Structural diversity of neuronal oxide synthase mRNA in the nervous  
 RT system.";  
 RL Biochem. Biophys. Res. Commun. 193:1014-1022(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM NNOS MU).  
 RC TISSUE=Skeletal muscle;

RX MEDLINE=96212184; PubMed=8626668;  
 RA Silveira F., Xia H., Bredt D.S.;  
 RT "Neuronal nitric-oxide synthase-mu, an alternatively spliced isoform  
 RT expressed in differentiated skeletal muscle.";  
 RL J. Biol. Chem. 271:11204-11208(1996).  
 RN [3]  
 RP ALTERNATIVE SPLICING (ISOFORMS NNOS BETA; NNOS GAMMA AND NNOS MU).  
 RX MEDLINE=97351924; PubMed=9208206;  
 RA Brennan J.E., Xia H., Chao D.S., Black S.M., Bredt D.S.;  
 RT "Regulation of neuronal nitric oxide synthase through alternative  
 RT transcripts.";  
 RL Dev. Neurosci. 19:224-231(1997).  
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN THE BRAIN AND  
 CC PERIPHERAL NERVOUS SYSTEM, NO DISPLAYS MANY PROPERTIES OF A  
 CC NEUROTRANSMITTER. ISOFORM NNOS MU MAY BE AN EFFECTOR ENZYME FOR  
 CC THE DYSTROPHIN COMPLEX.  
 CC -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) -> CITRULLINE +  
 CC NITRIC OXIDE + N NADP(+).  
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 CC TETRAHYDROBIPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 CC THE ENZYME (BY SIMILARITY).  
 CC -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN. INHIBITED BY  
 CC N-NOS-INHIBITING PROTEIN (PIN) WHICH MAY PREVENT THE DIMERIZATION  
 CC OF THE PROTEIN (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: IN SKELETAL MUSCLE, NNOS IS LOCALIZED  
 CC BENEATH THE SARCOLEMMMA OF FAST-TWITCH MUSCLE FIBER BY ASSOCIATING  
 CC WITH THE DYSTROPHIN GLYCOPROTEIN COMPLEX.  
 CC -1- ALTERNATIVE PRODUCTS: FIVE ISOFORMS; N-NOS-1 (SHOWN HERE), N-NOS-  
 CC 2, NNOS BETA, NNOS GAMMA AND NNOS MU/MUSCLE-SPECIFIC; ARE PRODUCED  
 CC BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE NERVOUS SYSTEM:  
 CC EXPRESSED IN CEREBRUM, OLFACTORY BULB, HIPPOCAMPUS, MIDBRAIN,  
 CC CEREBELLUM, PONS, MEDULLA OBLONGATA, AND SPINAL CORD. ALSO FOUND  
 CC IN SKELETAL MUSCLE, WHERE IT IS LOCALIZED BENEATH THE SARCOLEMMMA  
 CC OF FAST TWITCH MUSCLE FIBERS, AND IN SPLEEN, HEART, KIDNEY, AND  
 CC LIVER. N-NOS-1 AND N-NOS-2 ARE FOUND IN ALL PARTS OF THE NERVOUS  
 CC SYSTEM. NNOS BETA AND GAMMA OCCUR IN A REGION-SPECIFIC MANNER IN  
 CC THE BRAIN AND NNOS BETA EXPRESSION IS DEVELOPMENTALLY REGULATED.  
 CC NNOS MU IS ONLY FOUND IN MATURE SKELETAL AND CARDIAC MUSCLES.  
 CC -1- INDUCTION: BY CHOLINERGIC AGONISTS ACTING AT INOSITOL PHOSPHATE-  
 CC LINKED MUSCARINIC RECEPTORS IN CARDIAC MYOCYTES.  
 CC -1- DOMAIN: THE PDZ DOMAIN IN THE N-TERMINAL PART OF THE NEURONAL  
 CC ISOFORM PARTICIPATES IN PROTEIN-PROTEIN INTERACTION, AND IS  
 CC RESPONSIBLE FOR TARGETING NNOS TO SYNAPTIC MEMBRANES IN MUSCLES.  
 CC -1- DISEASE: IN MDX MICE (MOUSE MODEL OF DYSTROPHINOPATHY) THE  
 CC DYSTROPHIN COMPLEX IS DISRUPTED AND NNOS IS DISPLACED FROM  
 CC SARCOLEMMMA AND ACCUMULATES IN THE CYTOSOL.  
 CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; D14552; BAA03415.1; -;  
 CC EMBL; S81982; AAB36469.1; -;  
 CC HSSP; P29477; 2NOS.  
 CC MGD; MGI:97360; Nos1.  
 CC InterPro: IPR001094; -;  
 CC InterPro: IPR001433; -;  
 CC InterPro: IPR001478; -;  
 CC InterPro: IPR001709; -;  
 CC InterPro: IPR003097; -;  
 CC Pfam; PF00667; FAD\_binding; 1.  
 CC Pfam; PF00595; PDZ; 1.  
 CC Pfam; PF00175; oxidored\_fad; 1.  
 CC PRINTS; PR00369; FLAVODOXIN.

! FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN THE BRAIN AND

Query Match 75.7%; Score 78; DB 1; Length 1429;  
Best Local Similarity 77.8%; Pred. No. 3.8e-05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIVPFRSFQWRHDSQ 18  
DB 1252 GIAPFRSFQWRQFDIQH 1269

RESULT 11  
NOS1\_HUMAN  
ID NOS1\_HUMAN STANDARD; PRT; 1434 AA.  
AC P29475;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL  
DE NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS).  
GN NOS1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid:9606;  
RN [1]  
RS SEQUENCE FROM N.A. (ISOFORM N-NOS-1).  
RX MEDLINE=95105197; PubMed=7528745;  
RA Hall A.V., Antoniou H., Wang Y., Cheung A.H., Arbus A.M., Olson S.L.,  
RA Lu W.C., Kau C.-L., Marsden P.A.;  
RT "Structural organization of the human neuronal nitric oxide synthase  
gene (NOS1).";  
RT J. Biol. Chem. 269:33082-33090(1994).  
RN [2]  
RS SEQUENCE FROM N.A. (ISOFORMS N-NOS-1 AND N-NOS-2).  
RX TISSUE=Cerebellum;  
RX MEDLINE=94267447; PubMed=7515942;  
RA Fujisawa H., Ogura T., Kurashima Y., Yokoyama T., Yamashita J.,  
RA Esumi H.;  
RT "Expression of two types of nitric oxide synthase mRNA in human  
neuroblastoma cell lines.";  
RT J. Neurochem. 63:140-145(1994).  
RN [3]  
RS SEQUENCE FROM N.A. (ISOFORM N-NOS-1).  
RX TISSUE=Brain;  
RX MEDLINE=93131039; PubMed=7678401;  
RA Nakane M., Schmidt H.H.W., Pollock J.S., Foerstermann U., Murad F.;  
RT "Cloned human brain nitric oxide synthase is highly expressed in  
skeletal muscle.";  
RT FEBS Lett. 316:175-180(1993).  
RN [4]  
RS SEQUENCE FROM N.A. (ISOFORM N-NOS-1).  
RX TISSUE=Retina;  
RX MEDLINE=97034095; PubMed=8879752;  
RA Park C.-S., Gnanotli C., Park R., Krishna G.;  
RT "Neuronal isoform of nitric oxide synthase is expressed at low levels  
in human retina.";  
RT Cell. Mol. Neurobiol. 16:499-515(1996).  
RN [5]  
RS SEQUENCE FROM N.A. (ISOFORMS TN-NOS; TN-NOSB AND TEX2 INSERTION).  
RX TISSUE=Testis;  
RX MEDLINE=97269048; PubMed=9111048;  
RA Wang Y., Golligorsky M.S., Lin M., Wilcox J.N., Marsden P.A.;  
RT "A novel, testis-specific mRNA transcript encoding an NH2-terminal  
truncated nitric-oxide synthase.";  
RT J. Biol. Chem. 272:11392-11401(1997).  
CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN THE BRAIN AND  
CC PERIPHERAL NERVOUS SYSTEM, NO DISPLAYS MANY PROPERTIES OF A  
CC NEUROTRANSMITTER.  
CC -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +  
CC NITRIC OXIDE + N NADP(+).  
CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
CC THE ENZYME.

-1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN. INHIBITED BY  
N-NOS-INHIBITING PROTEIN (PIN) WHICH MAY PREVENT THE DIMERIZATION  
OF THE PROTEIN.  
-1- SUBUNIT: HOMODIMER.  
-1- SUBCELLULAR LOCATION: IN SKELETAL MUSCLE, IT IS LOCALIZED BENEATH  
THE SARCOLEMMMA OF FAST-TWITCH MUSCLE FIBER BY ASSOCIATING WITH THE  
DYSTROPHIN GLYCOPROTEIN COMPLEX.  
-1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: N-NOS-1 (SHOWN HERE), N-NOS-  
2, TN-NOS/TN-NOSB AND TEX2 INSERTION; ARE PRODUCED BY ALTERNATIVE  
SPLICING. TN-NOS/TN-NOSB ARE PRODUCED BY DIFFERENT ALTERNATIVE  
SPLICING EVENTS IMPLICATING EITHER THE UNTRANSLATED EXONS TEX1  
(TN-NOS) OR TEX1B (TN-NOSB) LEADING TO A NH2-TRUNCATED PROTEIN  
WHICH POSSESSES ENZYMIC ACTIVITY COMPARABLE TO THAT OF N-NOS-1.  
THE COOH-TRUNCATED TEX2 INSERTION ISOFORM IS PRODUCED BY INSERTION  
OF THE TEX2 EXON BETWEEN EXONS 3 AND 4 OF THE N-NOS-1 ISOFORM,  
LEADING TO A FRAMESHIFT AND A PREMATURE STOP CODON.  
-1- TISSUE SPECIFICITY: THE N-NOS-1 ISOFORM IS UBQUITOUSLY EXPRESSED:  
DETECTED IN SKELETAL MUSCLE AND BRAIN, ALSO IN TESTIS, LUNG AND  
KIDNEY, AND AT LOW LEVELS IN HEART, ADRENAL GLAND AND RETINA. NOT  
DETECTED IN THE PLATELETS. THE TN-NOS ISOFORM IS EXPRESSED ONLY IN  
TESTIS. THE TN-NOSB ISOFORM IS DETECTED AT LOW LEVELS ONLY IN THE  
TESTIS. THE TEX2 INSERTION ISOFORM IS DETECTED IN TESTIS, SKELETAL  
MUSCLE, LUNG, AND KIDNEY, AT LOW LEVELS IN THE BRAIN, BUT NOT IN  
THE HEART AND ADRENAL GLAND.  
-1- DOMAIN: THE PDZ DOMAIN IN THE N-TERMINAL PART OF THE NEURONAL  
ISOFORM PARTICIPATES IN PROTEIN-PROTEIN INTERACTION, AND IS  
RESPONSIBLE FOR TARGETING NNOS TO SYNAPTIC MEMBRANES IN MUSCLES  
(BY SIMILARITY).  
-1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
-1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; U17327; AAB62405.1; -  
EMBL; U17326; AAB60654.1; ALT\_SEQ.  
EMBL; U17299; AAB60654.1; JOINED.  
EMBL; U17300; AAB60654.1; JOINED.  
EMBL; U17301; AAB60654.1; JOINED.  
EMBL; U17302; AAB60654.1; JOINED.  
EMBL; U17303; AAB60654.1; JOINED.  
EMBL; U17304; AAB60654.1; JOINED.  
EMBL; U17305; AAB60654.1; JOINED.  
EMBL; U17307; AAB60654.1; JOINED.  
EMBL; U17308; AAB60654.1; JOINED.  
EMBL; U17309; AAB60654.1; JOINED.  
EMBL; U17310; AAB60654.1; JOINED.  
EMBL; U17311; AAB60654.1; JOINED.  
EMBL; U17312; AAB60654.1; JOINED.  
EMBL; U17313; AAB60654.1; JOINED.  
EMBL; U17314; AAB60654.1; JOINED.  
EMBL; U17315; AAB60654.1; JOINED.  
EMBL; U17316; AAB60654.1; JOINED.  
EMBL; U17317; AAB60654.1; JOINED.  
EMBL; U17318; AAB60654.1; JOINED.  
EMBL; U17319; AAB60654.1; JOINED.  
EMBL; U17320; AAB60654.1; JOINED.  
EMBL; U17321; AAB60654.1; JOINED.  
EMBL; U17322; AAB60654.1; JOINED.  
EMBL; U17323; AAB60654.1; JOINED.  
EMBL; U17324; AAB60654.1; JOINED.  
EMBL; U17325; AAB60654.1; JOINED.  
EMBL; D16408; BAA03895.1; -  
EMBL; L02881; AAA36376.1; -  
EMBL; U31466; AAB49040.1; -  
EMBL; U66362; -; NOT\_ANNOTATED\_CDS.  
PIR; S28878; S28878.  
HSSP; P00388; IAMO.



QY 1 GIVPRSFQORLHD 15  
 DB 982 GIAPRSEFQORLYD 996

RESULT 13  
 NOS3\_HUMAN  
 ID NOS3\_HUMAN STANDARD: PRT: 1202 AA.  
 AC P29474; Q14251; Q14434; Q13662;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE NITRIC-OXIDE SYNTHASE, ENDOTHELIAL (EC 1.14.13.39) (EC-NOS) (NOS, TYPE  
 DE III) (NOSIII) (ENDOTHELIAL NOS) (ENOS) (CONSTITUTIVE NOS) (CNOS).  
 GN NOS3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92340475; PubMed=1378832;  
 RA Janssens S.P., Shimouchi A., Quettermous T., Bloch D.B., Bloch K.D.;  
 RT "Cloning and expression of a cDNA encoding human endothelium-derived  
 RT relaxing factor/nitric oxide synthase.";  
 RL J. Biol. Chem. 267:14519-14522(1992).  
 RN [2]  
 RP ERRATUM.  
 RA Janssens S.P., Shimouchi A., Quettermous T., Bloch D.B., Bloch K.D.;  
 RL J. Biol. Chem. 267:22694-22694(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92354731; PubMed=1379542;  
 RA Marsden P.A., Schappert K.T., Chen H.S., Flowers M., Sundell C.L.,  
 RA Wilcox J.N., Lamas S., Michel T.;  
 RT "Molecular cloning and characterization of human endothelial nitric  
 RT oxide synthase.";  
 RL FEBS Lett. 307:287-293(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93325239; PubMed=7688726;  
 RA Marsden P.A., Heng H.H., Scherer S.W., Stewart R.J., Hall A.V.,  
 RA Shi X.M., Tsui L.C., Schappert K.T.;  
 RT "Structure and chromosomal localization of the human constitutive  
 RT endothelial nitric oxide synthase gene.";  
 RL J. Biol. Chem. 268:17478-17488(1993).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Umbilical vein;  
 RA Liao J.K.;  
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=94161710; PubMed=7509596;  
 RA Nadaud S.A., Bonardeaux A., Lathrop M., Soubrier F.;  
 RT "Gene structure, polymorphism and mapping of the human endothelial  
 RT nitric oxide synthase gene.";  
 RL Biochem. Biophys. Res. Commun. 198:1027-1033(1994).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94333373; PubMed=7519887;  
 RA Miyahara K., Kawamoto T., Sase K., Yui Y., Toda K., Yang L.X.,  
 RA Hattori R., Aoyama T., Yamamoto Y., Doi Y., Ogoshi S.,  
 RA Hashimoto K., Kawai C., Sasayama S., Shizuta Y.;  
 RT "Cloning and structural characterization of the human endothelial  
 RT nitric-oxide-synthase gene.";  
 RL Eur. J. Biochem. 223:719-726(1994).  
 RN [8]  
 RP SEQUENCE OF 1-52 FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=94245207; PubMed=7514568;

RA Robinson L.J., Weremowicz S., Morton C.C., Michel T.;  
 RT "Isolation and chromosomal localization of the human endothelial  
 RT nitric oxide synthase (NOS3) gene.";  
 RL Genomics 19:350-357(1994).  
 RN [9]  
 RP SEQUENCE OF 410-527 FROM N.A.  
 RC TISSUE=Platelet;  
 RX MEDLINE=96077182; PubMed=7475956;  
 RA Sase K., Michel T.;  
 RT "Expression of constitutive endothelial nitric oxide synthase in human  
 RT blood platelets.";  
 RL Life Sci. 57:2049-2055(1995).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
 RX MEDLINE=99173237; PubMed=10074942;  
 RA Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,  
 RA Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,  
 RA Weber P.C.;  
 RT "Structural characterization of nitric oxide synthase isoforms  
 RT reveals striking active-site conservation.";  
 RL Nat. Struct. Biol. 6:233-242(1999).  
 RN [11]  
 RP VARIANT CORONARY SPASM ASP-297.  
 RX MEDLINE=98407797; PubMed=9737779;  
 RA Yoshimura M., Yasue H., Nakayama M., Shimasaki Y., Sumida H.,  
 RA Sugiyama S., Kugiyama K., Ogawa H., Ogawa Y., Saito Y., Miyamoto Y.,  
 RA Nao K.;  
 RT "A missense Glu298Asp variant in the endothelial nitric oxide synthase  
 RT gene is associated with coronary spasm in the Japanese.";  
 RL Hum. Genet. 103:65-69(1998).  
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN  
 CC VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A GMP-MEDIATED SIGNAL  
 CC TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH  
 CC FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND  
 CC PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS.  
 CC -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) -> CITRULLINE +  
 CC NITRIC OXIDE + N NADP(+).  
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 CC TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 CC THE ENZYME.  
 CC -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- TISSUE SPECIFICITY: PLATELETS.  
 CC -1- DISEASE: DEFECTS IN NOS3 ARE INVOLVED IN CORONARY SPASM.  
 CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M93718; AAA36364.1; -;  
 DR EMBL; M95296; AAA36372.1; -;  
 DR EMBL; L10709; AAA36365.1; -;  
 DR EMBL; L10693; AAA36365.1; JOINED.  
 DR EMBL; L10694; AAA36365.1; JOINED.  
 DR EMBL; L10695; AAA36365.1; JOINED.  
 DR EMBL; L10696; AAA36365.1; JOINED.  
 DR EMBL; L10697; AAA36365.1; JOINED.  
 DR EMBL; L10698; AAA36365.1; JOINED.  
 DR EMBL; L10699; AAA36365.1; JOINED.  
 DR EMBL; L10700; AAA36365.1; JOINED.  
 DR EMBL; L10701; AAA36365.1; JOINED.  
 DR EMBL; L10702; AAA36365.1; JOINED.  
 DR EMBL; L10703; AAA36365.1; JOINED.  
 DR EMBL; L10704; AAA36365.1; JOINED.  
 DR EMBL; L10705; AAA36365.1; JOINED.  
 DR EMBL; L10706; AAA36365.1; JOINED.  
 DR EMBL; L10707; AAA36365.1; JOINED.  
 DR EMBL; L10708; AAA36365.1; JOINED.

DR EMBL: L26914; AAA36374.1; --  
DR EMBL: X76303; CAA53950.1; --  
DR EMBL: X76304; CAA53950.1; JOINED.  
DR EMBL: X76305; CAA53950.1; JOINED.  
DR EMBL: X76306; CAA53950.1; JOINED.  
DR EMBL: X76307; CAA53950.1; JOINED.  
DR EMBL: X76308; CAA53950.1; JOINED.  
DR EMBL: X76309; CAA53950.1; JOINED.  
DR EMBL: X76310; CAA53950.1; JOINED.  
DR EMBL: X76311; CAA53950.1; JOINED.  
DR EMBL: X76312; CAA53950.1; JOINED.  
DR EMBL: X76313; CAA53950.1; JOINED.  
DR EMBL: X76314; CAA53950.1; JOINED.  
DR EMBL: X76315; CAA53950.1; JOINED.  
DR EMBL: X76316; CAA53950.1; JOINED.  
DR EMBL: D26607; BAA05652.1; --  
DR EMBL: L23210; AAA36373.1; --  
DR EMBL: S80791; AAD14336.1; --  
DR PIR: S24052; S24052.  
DR PIR: A42867; A42867.  
DR PDB: 3NOS; 04-FEB-00.  
DR MIM: 163729; --  
DR InterPro: IPR001094; --  
DR InterPro: IPR001433; --  
DR InterPro: IPR001709; --  
DR InterPro: IPR003097; --  
DR Pfam: PF00667; FAD\_binding; 1.  
DR Pfam: PF00175; oxidored\_fad; 1.  
DR PRINTS: PR00369; FLAVODOXIN.  
DR PRINTS: PR00371; FPNCR.  
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;  
KW Lipoprotein; Palmitate; Disease mutation; Calcium-binding; Heme;  
KW Zinc; Metal-binding; Multigene family; 3D-structure.  
FT INIT\_MET 0  
FT BINDING 183 183 HEME (BY SIMILARITY).  
FT DOMAIN 490 509 CALMODULIN-BINDING (POTENTIAL).  
FT NP\_BIND 648 679 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
FT NP\_BIND 792 803 FAD (ADP PART) (BY SIMILARITY).  
FT NP\_BIND 934 944 FAD (FLAVIN PART) (BY SIMILARITY).  
FT NP\_BIND 1009 1027 NADP (RIBOSE PART) (BY SIMILARITY).  
FT NP\_BIND 1107 1122 NADP (ADP PART) (BY SIMILARITY).  
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).  
FT LIPID 14 14 PALMITATE (BY SIMILARITY).  
FT LIPID 25 25 PALMITATE (BY SIMILARITY).  
FT METAL 93 93 ZINC.  
FT METAL 98 98 ZINC.  
FT VARIANT 297 297 E -> D (IN CORONARY SPASM).  
FT FTIG=VAR\_008037.  
FT CONFLICT 52 52 S -> R (IN REF. 8).  
FT CONFLICT 488 488 G -> S (IN REF. 9).  
FT CONFLICT 566 566 V -> W (IN REF. 6).  
FT CONFLICT 1149 1149 R -> Q (IN REF. 7).  
FT CONFLICT 1193 1193 D -> E (IN REF. 6).  
SQ SEQUENCE 1202 AA; 133157 MW; 93D127D6C14AC92E CRC64;  
  
Query Match 72.8%; Score 75; DB 1; Length 1202;  
Best Local Similarity 80.0%; Pred. No. 0.0001;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 GIVPFRFWOORLHD 15  
Db 1016 GIAPFRFWOERLHD 1030  
  
RESULT 14  
ID NOS3\_BOVIN STANDARD; PRT; 1204 AA.  
AC P29473;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE NITRIC-OXIDE SYNTHASE, ENDOTHELIAL (EC 1.14.13.39) (EC-NOS) (NOS, TYPE

DE III) (NOSIII) (ENDOTHELIAL NOS) (ENOS) (CONSTITUTIVE NOS) (CNOS).  
GN NOS3.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92335295; PubMed=1378626;  
RA Lamas S., Marsden P.A., Li G.K., Tempst P., Michel T.;  
RT "Endothelial nitric oxide synthase: molecular cloning and  
characterization of a distinct constitutive enzyme isoform.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:6348-6352(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93055452; PubMed=1385480;  
RA Nishida K., Harrison D.G., Navas J.P., Fisher A.A., Dockery S.P.,  
RA Uematsu M., Nerem R.M., Alexander R.W., Murphy T.J.;  
RT "Molecular cloning and characterization of the constitutive bovine  
aortic endothelial cell nitric oxide synthase.";  
RL J. Clin. Invest. 90:2092-2096(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Aortic endothelium;  
RX MEDLINE=92348367; PubMed=1379225;  
RA Sessa W.C., Harrison J.K., Barber C.M., Zeng D., Durieux M.E.,  
RA D'Angelo D.D., Lynch K.R., Peach M.J.;  
RT "Molecular cloning and expression of a cDNA encoding endothelial cell  
nitric oxide synthase.";  
RL J. Biol. Chem. 267:15274-15276(1992).  
RN [4]  
RP MYRISTOYLATION.  
RX MEDLINE=93231982; PubMed=7682550;  
RA Busconi L., Michel T.;  
RT "Endothelial nitric oxide synthase. N-terminal myristoylation  
determines subcellular localization.";  
RL J. Biol. Chem. 268:8410-8413(1993).  
RN [5]  
RP PALMITOYLATION.  
RX MEDLINE=96102197; PubMed=8524847;  
RA Robinson L.J., Michel T.;  
RT "Mutagenesis of palmitoylation sites in endothelial nitric oxide  
synthase identifies a novel motif for dual acylation and subcellular  
targeting.";  
RL Proc. Natl. Acad. Sci. U.S.A. 92:11776-11780(1995).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 66-481.  
RX MEDLINE=99091052; PubMed=9875848;  
RA Raman C.S., Li H., Martasek P., Kral V., Masters B.S., Poulos T.L.;  
RT "Crystal structure of constitutive endothelial nitric oxide synthase:  
a paradigm for pterin function involving a novel metal center.";  
RL Cell 95:939-950(1998).  
CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN  
VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A CGMP-MEDIATED SIGNAL  
TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH  
FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND  
PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS.  
CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +  
NITRIC OXIDE + N NADP(+).  
CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
THE ENZYME.  
CC -!- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN.  
CC -!- SUBUNIT: HOMODIMER.  
CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

```

CC EMBL; M99057; AAA30567.1; -.
CC EMBL; M89952; AAA30494.1; -.
DR EMBL; M95674; AAA30669.1; -.
DR PDB; 1NSE; 18-MAY-99.
DR PDB; 2NSE; 25-MAY-99.
DR PDB; 3NSE; 18-MAY-99.
DR PDB; 4NSE; 18-MAY-99.
DR InterPro; IPR001094; -.
DR InterPro; IPR001433; -.
DR InterPro; IPR001709; -.
DR InterPro; IPR003097; -.
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00175; oxidored_fad; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;
KW Lipoprotein; Palmitate; Phosphorylation; Calcium-binding; Heme;
KW Zinc; Metal-binding; Multigene family; 3D-structure.
FT INIT_MET 0
FT BINDING 185 185 HEME (BY SIMILARITY).
FT DOMAIN 491 511 CALMODULIN-BINDING (POTENTIAL).
FT NP_BIND 650 681 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 794 805 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 936 946 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 1011 1029 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 1109 1124 NADP (ADP PART) (BY SIMILARITY).
FT LIPID 1 1 MYRISTATE.
FT LIPID 14 14 PALMITATE.
FT LIPID 25 25 PALMITATE.
FT METAL 95 95 ZINC.
FT MOD_RES 100 100 ZINC.
FT MOD_RES 142 142 PHOSPHORYLATION (BY CAPK).
FT CONFLICT 99 99 C -> R (IN REF. 3).
FT CONFLICT 164 164 Y -> I (IN REF. 3).
FT CONFLICT 317 327 EHPTLEWFAAL -> GAPHTGVVRGP (IN REF. 3).
FT CONFLICT 454 454 S -> Y (IN REF. 3).
FT CONFLICT 458 458 T -> P (IN REF. 3).
FT CONFLICT 740 740 T -> A (IN REF. 3).
FT CONFLICT 803 804 CP -> SA (IN REF. 3).
FT CONFLICT 856 856 L -> V (IN REF. 3).
FT CONFLICT 906 907 WF -> LV (IN REF. 3).
FT CONFLICT 1041 1041 A -> H (IN REF. 3).
SQ SEQUENCE 1204 AA; 133155 MW; D017210062ABE4B0 CRC64;

Query Match 72.8%; Score 75; DB 1; Length 1204;
Best Local Similarity 80.0%; Pred. No. 0.0001;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GIVPFRSFQQRRLHD 15
Db 1018 GIAPFRGFQERLHD 1032

RESULT 15
NOS3_PIG STANDARD; PRT; 1204 AA.
AC Q28969;
DC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NITRIC-OXIDE SYNTHASE, ENDOTHELIAL (EC 1.14.13.39) (EC-NOS) (NOS, TYPE III) (NOSIII) (ENDOTHELIAL NOS) (ENOS) (CONSTITUTIVE NOS) (CNOS).
GN NOS3 OR NOS.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Sulina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RC SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=pulmonary artery;

```

```

RX MEDLINE=97293429; PubMed=9149402;
RA Zhang J., Patel J.M., Block E.R.;
RT "Molecular cloning, characterization and expression of a nitric oxide
synthase from porcine pulmonary artery endothelial cells.";
RL Comp. Biochem. Physiol. 116B:485-491(1997).
RN [2]
RP SEQUENCE OF 1031-1205 FROM N.A.
RA Patel J.M., Block E.R.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN
CC VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A GMP-MEDIATED SIGNAL
CC TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH
CC FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND
CC PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) - CITRULLINE +
CC NITRIC OXIDE + N NADP(+).
CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME (BY SIMILARITY).
CC -!- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY
CC SIMILARITY).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- INDUCTION: REPRESSED BY PROINFLAMMATORY CYTOKINES.
CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U59924; AAB39539.1; -.
DR EMBL; U33832; AAB4933.1; -.
DR HSSP; P29477; 2NOS.
DR InterPro; IPR001094; -.
DR InterPro; IPR001433; -.
DR InterPro; IPR001709; -.
DR InterPro; IPR003097; -.
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00175; oxidored_fad; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;
KW Lipoprotein; Palmitate; Calcium-binding; Heme; Zinc; Metal-binding;
KW Multigene family.
FT INIT_MET 0
FT BINDING 185 185 HEME (BY SIMILARITY).
FT DOMAIN 491 511 CALMODULIN-BINDING (POTENTIAL).
FT NP_BIND 650 681 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 794 805 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 936 946 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 1011 1029 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 1109 1124 NADP (ADP PART) (BY SIMILARITY).
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
FT LIPID 14 14 PALMITATE (BY SIMILARITY).
FT LIPID 25 25 PALMITATE (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 100 100 ZINC (BY SIMILARITY).
SQ SEQUENCE 1204 AA; 133274 MW; 48676BA95DB14CFE CRC64;

Query Match 72.8%; Score 75; DB 1; Length 1204;
Best Local Similarity 80.0%; Pred. No. 0.0001;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GIVPFRSFQQRRLHD 15
Db 1018 GIAPFRGFQERLHD 1032

```



Search completed: September 10, 2001, 14:09:51  
Job time: 560 sec

---

**This Page Blank (aspt0)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 13:57:41 ; Search time 42.28 Seconds  
(without alignments)  
32.430 Million cell updates/sec

Title: US-08-833-506C-25

Perfect score: 103

Sequence: 1 GIVPFRSFQWQRLHDSOH 18

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	96.1	1144	1 A43271	nitric-oxide synth
2	99	96.1	1147	1 S47647	nitric-oxide synth
3	99	96.1	1147	1 I56575	nitric-oxide synth
4	99	96.1	1147	1 S38253	nitric-oxide synth
5	99	96.1	1147	2 JC5027	nitric-oxide synth
6	99	96.1	1147	2 JC5028	nitric-oxide synth
7	99	96.1	1147	2 JC5029	nitric-oxide synth
8	99	96.1	1147	2 S65440	nitric-oxide synth
9	99	96.1	1153	2 A49676	nitric-oxide synth
10	91	88.3	1147	1 I53165	nitric-oxide synth
11	86	83.5	69	2 I39204	nitric-oxide synth
12	79	76.7	136	2 I46074	nitric-oxide synth
13	78	75.7	1429	2 JN0609	nitric-oxide synth
14	78	75.7	1429	2 S16233	nitric-oxide synth
15	78	75.7	1433	2 G01946	nitric-oxide synth
16	75	72.8	1203	1 A47501	nitric-oxide synth
17	75	72.8	1205	1 A38943	nitric-oxide synth
18	73	70.9	1202	2 S71424	nitric-oxide synth
19	69	67.0	1153	2 T31080	nitric-oxide synth
20	63	61.2	63	2 I51917	nitric-oxide synth
21	57	55.3	1247	2 T31331	nitric-oxide synth
22	56	54.4	1206	2 T30555	nitric-oxide synth
23	56	54.4	1350	2 T13254	nitric-oxide synth
24	53	51.5	601	2 F84979	sulfite reductase
25	52	50.5	599	1 A34231	sulfite reductase
26	52	50.5	599	1 H65057	sulfite reductase
27	52	50.5	599	2 D85926	hypothetical prote
28	51	49.5	346	2 S72222	ferredoxin--NADP+
29	51	49.5	354	2 T08035	ferredoxin--NADP+

30	49	47.6	267	2 C83919	hypothetical prote
31	48	46.6	605	1 G70040	sulfite reductase
32	48	46.6	607	2 A83726	sulfite reductase
33	47	45.6	614	2 B82329	sulfite reductase
34	47	45.6	699	2 T14904	NADPH--ferrihemopr
35	47	45.6	705	2 T10723	NADPH--ferrihemopr
36	46	44.7	506	2 S37156	NADPH--ferrihemopr
37	46	44.7	583	2 T50103	probable oxidoredu
38	46	44.7	590	2 S37157	NADPH--ferrihemopr
39	46	44.7	604	2 E81905	NADPH--ferrihemopr
40	46	44.7	604	2 H81110	sulfite reductase
41	46	44.7	692	2 S37159	NADPH--ferrihemopr
42	46	44.7	711	2 T14081	NADPH--ferrihemopr
43	46	44.7	712	2 S21531	NADPH--ferrihemopr
44	46	44.7	713	2 JE0230	NADPH--cytochrome P
45	46	44.7	714	1 S31502	NADPH--ferrihemopr

ALIGNMENTS

RESULT 1

A43271  
nitric-oxide synthase (EC 1.14.13.39), calmodulin-independent - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Mar-2000  
C:Accession: A43271; A42166; JN0458; A46186  
R:Xie, Q.; Cho, H.J.; Calaycay, J.; Mumford, R.A.; Swiderek, K.M.; Lee, T.D.; Ding, A  
Science 256, 225-228, 1992  
A:Title: Cloning and characterization of inducible nitric oxide synthase from mouse m  
A:Reference number: A43271; MUID:92229444  
A:Accession: A43271  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1144 <XIE>  
A:Cross-references: GB:M87039; NID:q198406; PIDN:AAA39315.1; PID:q198407  
R:Lyons, C.R.; Orloff, G.J.; Cunningham, J.M.  
J. Biol. Chem. 267, 6370-6374, 1992  
A:Title: Molecular cloning and functional expression of an inducible nitric oxide syn  
A:Reference number: A42166; MUID:92210618  
A:Accession: A42166  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1144 <LYO>  
A:Cross-references: GB:M84373; NID:q200095; PIDN:AAA39834.1; PID:q200096  
R:Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.  
Biochem. Biophys. Res. Commun. 191, 767-774, 1993  
A:Title: Hepatocytes and macrophages express an identical cytokine inducible nitric o

A:Reference number: JN0457; MUID:93221515  
A:Accession: JN0458  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-278,'F',280-682,'H',684-937,939-1144 <WOO>  
A:Experimental source: liver  
R:Lowenstein, C.J.; Glatt, C.S.; Bredt, D.S.; Snyder, S.H.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6711-6715, 1992  
A:Title: Cloned and expressed macrophage nitric oxide synthase contrasts with the bra  
A:Reference number: A46186; MUID:92357701  
A:Accession: A46186  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-190,'V',192-765,'P',767-843,'G',845-1144 <LOW>  
A:Cross-references: GB:M92649; NID:q200109  
A:Experimental source: BALB/c, RAW 264.7 cells, macrophage  
A:Note: sequence extracted from NCBI backbone (NCBIP:113541)  
C:Genetics:  
A:Gene: NOS  
C:Function:  
A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NAD  
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprtein re  
C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me  
F:533-1121/Domain: NADPH--ferrihemoprtein reductase homology <FEH>  
F:535-671/Domain: flavodoxin homology <FLX>

C; keywords: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reductase; superfamily A; experimental source: kidney

F:191-199/Domain: heme-binding #status predicted <HMB>  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:620-647/Domain: FMN binding #status predicted <FMN>  
 F:764-775,899-910/Domain: FAD binding #status predicted <FAD>  
 F:975-993,1054-1067/Domain: NADP binding #status predicted <NDP>  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 96.1%; Score 99; DB 2; Length 1147;  
 Best Local Similarity 94.4%; Pred. No. 8.2e-08;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVPFRSFQOORLHDSQH 18  
 || |||||  
 Db 982 GIAPFRSFQOORLHDSQH 999

RESULT 6  
 JC5028  
 nitric-oxide synthase (EC 1.14.13.39) L - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 04-Mar-2000  
 C:Accession: JC5028  
 R:Tsutsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, M  
 Biol. Pharm. Bull. 19, 1374-1376, 1996  
 A:Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and u  
 A:Reference number: JC5027; MUID:97070590  
 A:Accession: JC5028  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <TSU>  
 A:Experimental source: lung  
 C:Comment: This protein synthesizes nitric oxide from L-arginine.  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein red  
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 96.1%; Score 99; DB 2; Length 1147;  
 Best Local Similarity 94.4%; Pred. No. 8.2e-08;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVPFRSFQOORLHDSQH 18  
 || |||||  
 Db 982 GIAPFRSFQOORLHDSQH 999

RESULT 7  
 JC5029  
 nitric-oxide synthase (EC 1.14.13.39), U - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 04-Mar-2000  
 C:Accession: JC5029  
 R:Tsutsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, M  
 Biol. Pharm. Bull. 19, 1374-1376, 1996  
 A:Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and u  
 A:Reference number: JC5027; MUID:97070590  
 A:Accession: JC5029  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <TSU>  
 A:Experimental source: uterus  
 C:Comment: This protein synthesizes nitric oxide from L-arginine.  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein red  
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 96.1%; Score 99; DB 2; Length 1147;  
 Best Local Similarity 94.4%; Pred. No. 8.2e-08;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVPFRSFQOORLHDSQH 18  
 || |||||  
 Db 982 GIAPFRSFQOORLHDSQH 999

RESULT 8  
 S65440  
 nitric-oxide synthase (EC 1.14.13.39) - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 04-Mar-2000  
 C:Accession: S65440  
 R:Iwashina, M.; Hirata, Y.; Imai, T.; Sato, K.; Marumo, F.  
 Eur. J. Biochem. 237, 668-673, 1996  
 A:Title: Molecular cloning of endothelial, inducible nitric oxide synthase gene from  
 A:Reference number: S65440; MUID:96235231  
 A:Accession: S65440  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <IWA>  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein re  
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me  
 F:506-535/Region: calmodulin binding  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:599-618/Region: biopterin binding  
 F:620-647/Region: FMN binding #status predicted  
 F:764-775/Region: FAD binding #status predicted  
 F:901-910/Region: FAD binding #status predicted  
 F:975-993/Region: NADPH binding #status predicted  
 F:1074-1087/Region: NADPH binding #status predicted  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 96.1%; Score 99; DB 2; Length 1147;  
 Best Local Similarity 94.4%; Pred. No. 8.2e-08;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVPFRSFQOORLHDSQH 18  
 || |||||  
 Db 982 GIAPFRSFQOORLHDSQH 999

RESULT 9  
 A49676  
 nitric-oxide synthase (EC 1.14.13.39), inducible - human  
 C:Species: Homo sapiens (man)  
 C:Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 20-Jun-2000  
 C:Accession: A49676; JX0345; G01947; I38933; S47566; A47475  
 R:Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; Hall, V.S.;  
 Proc. Natl. Acad. Sci. U.S.A. 90, 11419-11423, 1993  
 A:Title: Cloning, characterization, and expression of a cDNA encoding an inducible ni  
 A:Reference number: A49676; MUID:94068614  
 A:Accession: A49676  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1153 <RES>  
 A:Cross-references: EMBL:X73029; NID:g441452; PIDN:CAA51512.1; PID:g441453  
 R:Hokari, A.; Zeniya, M.; Esumi, H.  
 J. Biochem. 116, 575-581, 1994  
 A:Title: Cloning and functional expression of human inducible nitric oxide synthase (  
 A:Reference number: JX0345; MUID:95155267  
 A:Accession: JX0345  
 A:Molecule type: mRNA  
 A:Residues: 1-607, L', 609-1153 <HOK>  
 A:Cross-references: DBJ:D26525; NID:g559326; PIDN:BAA05531.1; PID:g1228940  
 A:Experimental source: glioblastoma cell line A-172  
 R:Park, C.; Park, R.; Krishna, G.  
 submitted to the EMBL Data Library, July 1995  
 A:Reference number: G08912



A:Reference number: JC2471; MUID:95126979  
A:Accession: JC2471  
A:Molecule type: protein  
C:Species: Homo sapiens (man)  
R:Seo, H.G.; Tatsumi, H.; Fujii, J.; Nishikawa, A.; Suzuki, K.; Kangawa, K.; Taniguchi, Y.  
J. Biochem. 115, 602-607, 1994  
A:Title: Nitric oxide synthase from rat colorectum: Purification, peptide sequencing,  
A:Reference number: PC2184; MUID:94334309  
A:Accession: PC2184  
A:Molecule type: protein  
A:Residues: 119-129;132-142;144-156;189-200;264-268,'V',270-276;305-310;360-369;376-384  
A:Experimental source: colorectum  
C:Comment: This protein is a cell signaling agent in the cardiovascular, central and peripheral nervous systems.  
C:Superfamily: GFGE domain homology; flavodoxin homology; NADPH--ferrihemoprotein redox homology;  
C:Keywords: calcium binding; calmodulin binding; chromoprotein; flavoprotein; heme; i-heme;  
F:23-95/Domain: GFGE domain homology <GLG>  
F:725-745/Region: calmodulin binding #status predicted  
F:750-769/Region: biotin binding #status predicted  
F:755-1394/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
F:757-935/Domain: flavodoxin homology <FLX>  
F:881-915/Region: FMN binding #status predicted  
F:1027-1038/Region: FAD binding #status predicted  
F:1245-1263/Region: NADP binding #status predicted  
F:415/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 75.7%; Score 78; DB 2; Length 1429;  
Best Local Similarity 77.8%; Pred. No. 0.00024;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIVFRSFQQRLHDSQH 18  
||| ||||||||| |  
Db 1252 GIAPFRSFWQQRFDIQH 1269

RESULT 15  
G01946  
nitric-oxide synthase (EC 1.14.13.39), neuronal - human  
N:Alternate names: nitric oxide synthase 1  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1996 #sequence-revision 06-Jun-1997 #text\_change 04-Mar-2000  
C:Accession: G01946; I56508; S28878  
R:Park, C.; Gianotti, C.; Park, R.; Krishna, G.  
submitted to the EMBL Data Library, July 1995  
A:Reference number: G08911  
A:Accession: G01946  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-1433 <PAR>  
A:Cross-references: EMBL:U931466; NID:g9513138; PIDN:AAB49040.1; PTD:g9513139  
R:Fujisawa, H.; Ogura, T.; Kurashima, Y.; Yokoyama, T.; Yamashita, J.; Esumi, H.  
J. Neurochem. 63, 140-145, 1994  
A:Title: Expression of two types of nitric oxide synthase mRNA in human neuroblastoma  
A:Reference number: I56508; MUID:94267447  
A:Accession: I56508  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-130,'K',132-177,'LA',179,'Rp',182,'G',184-1433 <RES>  
A:Cross-references: GB:D16408; NID:g506339; PIDN:BAA03895.1; PID:g987662  
R:Nakane, M.; Schmidt, H.H.W.; Pollock, J.S.; Foerstermann, U.; Murad, F.  
FEBS Lett. 316, 175-180, 1993  
A:Title: Cloned human brain nitric oxide synthase is highly expressed in skeletal muscle  
A:Reference number: S28878; MUID:93131039  
A:Accession: S28878  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-130,'K',132-490,'HR',493-547,'L',549-561,'A',563-1362,'I',1364-1405,'I'  
A:Cross-references: GB:L02881; NID:g189261  
C:Genetics:  
A:Gene: GDB:NOS1; NOS  
A:Cross-references: GDB:132579; OMIM:163731  
A:Map position: 12q24.2-12q24.31  
C:Superfamily: GFGE domain homology; flavodoxin homology; NADPH--ferrihemoprotein redox homology

C:Keywords: chromoprotein; flavoprotein; heme; iron; metalloprotein; oxidoreductase  
 F:23-95/Domain: GLGF domain homology <GLG>  
 F:759-1398/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:761-939/Domain: flavodoxin homology <FLX>  
 F:419/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 75.7%; Score 78; DB 2; Length 1433;  
 Best Local Similarity 77.8%; Pred. No. 0.00024;  
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 GIVPPRSFWQQRLLHDSQH 18  
 II IIIIIII I II  
 Db 1256 GIAPPFSFWQQRQFDIQH 1273

Search completed: September 10, 2001, 14:01:13  
 Job time: 212 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 13:58:11 ; Search time 35.97 Seconds  
(without alignments)  
10.304 Million cell updates/sec

Title: US-08-833-506C-25

Perfect score: 103

Sequence: 1 GIVPFRSFQORLHDSQH 18

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

1: /cgn2\_6/ptodata/2/1aa/5A-COMB.pap.\*

2: /cgn2\_6/ptodata/2/1aa/5B-COMB.pap.\*

3: /cgn2\_6/ptodata/2/1aa/6A-COMB.pap.\*

4: /cgn2\_6/ptodata/2/1aa/6B-COMB.pap.\*

5: /cgn2\_6/ptodata/2/1aa/PCTUS-COMB.pap.\*

6: /cgn2\_6/ptodata/2/1aa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	100.0	1153	1	US-08-314-917-2
2	103	100.0	1153	1	US-08-265-046-2
3	103	100.0	1153	2	US-08-465-522-2
4	103	100.0	1153	5	PCT-US93-11401-2
5	103	100.0	1153	5	PCT-US95-07849-2
6	99	96.1	1144	1	US-08-147-812-5
7	99	96.1	1144	2	US-08-319-866-12
8	99	96.1	1144	4	US-09-123-708-2
9	99	96.1	1144	4	US-09-123-624-2
10	99	96.1	1146	4	US-09-126-109-12
11	78	75.7	1429	1	US-07-642-002-2
12	78	75.7	1429	2	US-08-365-486A-13
13	78	75.7	1429	2	US-08-319-866-11
14	78	75.7	1429	4	US-08-880-342-13
15	78	75.7	1430	2	US-08-705-625-4
16	78	75.7	1430	3	US-09-010-998-5
17	78	75.7	1430	4	US-09-220-574-4
18	78	75.7	1433	2	US-08-365-486A-21
19	78	75.7	1433	4	US-09-123-708-4
20	78	75.7	1433	4	US-09-123-624-4
21	78	75.7	1433	4	US-08-880-342-21
22	78	75.7	1434	2	US-08-365-486A-19
23	78	75.7	1434	4	US-08-880-342-19
24	78	75.7	1554	2	US-08-705-625-3
25	78	75.7	1554	3	US-09-010-998-6
26	78	75.7	1554	4	US-09-220-574-3
27	78	75.7	1554	1	US-07-908-245-2

28 75 72.8 1205 2 US-08-319-866-10 Sequence 10, Appl  
29 75 72.8 1205 4 US-09-123-708-6 Sequence 6, Appl  
30 75 72.8 1205 4 US-09-123-708-6 Sequence 6, Appl  
31 56 54.4 1350 2 US-08-319-866-9 Sequence 9, Appl  
32 44 42.7 308 2 US-09-047-026A-23 Sequence 23, Appl  
33 44 42.7 3177 2 US-08-477-451-4 Sequence 4, Appl  
34 42 40.8 417 1 US-08-553-703A-2 Sequence 2, Appl  
35 42 40.8 417 2 US-09-006-021-2 Sequence 2, Appl  
36 42 40.8 419 1 US-08-553-703A-3 Sequence 3, Appl  
37 42 40.8 419 2 US-09-006-021-3 Sequence 3, Appl  
38 42 40.8 693 1 US-08-553-279-2 Sequence 2, Appl  
39 41 39.8 872 3 US-08-337-797A-2 Sequence 2, Appl  
40 41 39.8 872 3 US-09-258-523-2 Sequence 2, Appl  
41 40 38.8 299 2 US-09-047-026A-24 Sequence 24, Appl  
42 40 38.8 408 2 US-08-924-847A-2 Sequence 2, Appl  
43 40 38.8 408 3 US-09-120-052-2 Sequence 2, Appl  
44 40 38.8 475 2 US-08-272-255-13 Sequence 13, Appl  
45 40 38.8 475 5 PCT-US95-08565-13 Sequence 13, Appl

#### ALIGNMENTS

RESULT 1  
US-08-314-917-2  
; Sequence 2, Application US/08314917  
; Patent No. 5468630  
; GENERAL INFORMATION:  
; APPLICANT: Billiar, Timothy R.  
; APPLICANT: Nussler, Andreas K.  
; APPLICANT: Geller, David A.  
; APPLICANT: Simmons, Richard L.  
; TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Arnold B. Silverman  
; ADDRESSEE: Eckert Seamans Cherin & Mellott  
; STREET: 600 Grant Street, 42nd Floor  
; CITY: Pittsburgh  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 15219  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/314,917  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/981,344  
; FILING DATE: 25-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Silverman, Arnold B.  
; REGISTRATION NUMBER: 22,614  
; REFERENCE/DOCKET NUMBER: 116972  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (412) 566-6000  
; TELEFAX: (412) 566-6099  
; TELEX: 866172  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1153 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-314-917-2

Query Match 100.0%; Score 103; DB 1; Length 1153;

Best Local Similarity	100.0%	Pred. No.	4.8e-09;
Matches	18;	Conservative	0;
		Mismatches	0;
		Indels	0;
		Gaps	0;

```

QY      1 GIVPERSFWQRLHDSQH 18
      {
Db     985 GIVPERSFWQRLHDSQH 10

```

Db 985 GIVPSEFWQORLHDSQH 1002

```

RESULT      2
US-08-265-046-2
; Sequence 2, Application US/08265046
; Patent No. 5658565
; GENERAL INFORMATION:
; APPLICANT: Timothy R. Billiar
; APPLICANT: Edith Tzeng
; APPLICANT: Andreas K. Nussler
; APPLICANT: David A. Geller
; APPLICANT: Richard L. Simmons
; TITLE OF INVENTION: Inducible Nitric Oxide Synthase
; TITLE OF INVENTION: Gene for Treatment of Disease
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
;

```

```
Query Match      100.0%; Score 103; DB 1; Length 1153;
Best Local Similarity 100.0%; Pred. No. 4.8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	GIVPFRSEWQORLHDSQH	18
Dp	985	GIVPFRSEWQORLHDSQH	1002

Db 985 GIVPSEWOORLHDSOH 1002

RESULT 3  
US-08-463-522-2  
; Sequence 2, Application US/08465522  
; Patent No. 5882908  
; GENERAL INFORMATION:  
; APPLICANT: Billiar, Timothy R.  
; APPLICANT: Nussler, Andreas K.  
; APPLICANT: Geller, David A.  
; APPLICANT: Simmons, Richard L.

```

: TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric
: TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lewis F. Gould, Jr.
: ADDRESSEE: Eckert Seamans Cherin & Mellott
: STREET: 1700 Market St. Suite 3232
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/465,522

```

Query Match	100.00;	Score 103;	DB 2;	Length 1153;
Best Local Similarity	100.00;	pred. NO. 4.8e-09;		
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 GIVPFRSEWQORLHDSQH 18  
|||  
Db 985 GIVPFRSEWQORLHDSQH 1002

db 985 GIVPFRSEWOORLHDSOH 1002

```

RESULT      4
;
; PCT-US93-111401-2
; Sequence 2, Application PCTUS93111401
; GENERAL INFORMATION:
; APPLICANT: Billiar, Timothy R.
; APPLICANT: Nussler, Andreas K.
; APPLICANT: Geller, David A.
; APPLICANT: Slimmons, Richard L.
; TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric
; TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
;

```

```

7 ZIP: 15219
7 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
7 OPERATING SYSTEM: PC-DOS/MS-DOS
7 SOFTWARE: PatentIn Release #1.0, Version #1.25
7 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: PCT/US93/11401
7 FILING DATE: 25-NOV-1992

```

```
?  
?  
? COUNTRY: USA  
? ZIP: 15219  
?  
? COMPUTER READABLE FORM:  
? MEDIUM TYPE: Floppy disk  
? COMPUTER: IBM PC Compatible  
? OPERATING SYSTEM: PC-DOS/MS-DOS  
? SOFTWARE: Patent In Release #1.0, Version #1.25  
? CURRENT APPLICATION DATA:  
? APPLICATION NUMBER: PCT/US93/11401  
? FILING DATE: 25-NOV-1992  
?
```

STATE: PA

```
?  
?  
? COUNTRY: USA  
? ZIP: 15219  
?  
? COMPUTER READABLE FORM:  
? MEDIUM TYPE: Floppy disk  
? COMPUTER: IBM PC Compatible  
? OPERATING SYSTEM: PC-DOS/MS-DOS  
? SOFTWARE: Patent In Release #1.0, Version #1.25  
? CURRENT APPLICATION DATA:  
? APPLICATION NUMBER: PCT/US93/11401  
? FILING DATE: 25-NOV-1992
```

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/981,344  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Silverman, Arnold B.  
REGISTRATION NUMBER: 22,614  
REFERENCE/DOCKET NUMBER: 116972  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (412) 566-6000  
TELEFAX: (412) 566-6099  
TELEX: 866172  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1153 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-11401-2

Query Match 100.0%; Score 103; DB 5; Length 1153;  
Best Local Similarity 100.0%; Pred. No. 4.8e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVPFRSFQOQLHDSQH 18  
|||

Db 985 GIVPFRSFQOQLHDSQH 1002

RESULT 5  
PCT-US95-07849-2  
SEQUENCE 2, Application PC/TUS9507849  
GENERAL INFORMATION:  
APPLICANT: University of Pittsburgh of the Commonwealth System of Higher  
EDUCATION  
TITLE OF INVENTION: Inducible Nitric Oxide Synthase  
NUMBER OF INVENTION: 2  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lewis F. Gould, Jr.  
ADDRESSEE: Eckert Seamans Cherin & Mellott  
STREET: 1700 Market Street, Suite 3232  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/07849  
FILING DATE:

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gould, Lewis F. Jr.  
REGISTRATION NUMBER: 25,057  
REFERENCE/DOCKET NUMBER: 119130-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 575-6020  
TELEFAX: (215) 575-6015  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1153 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-07849-2

Query Match 100.0%; Score 103; DB 5; Length 1153;  
Best Local Similarity 100.0%; Pred. No. 4.8e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVPFRSFQOQLHDSQH 18  
|||

Db 985 GIVPFRSFQOQLHDSQH 1002

RESULT 6  
US-08-147-812-5  
SEQUENCE 5, Application US/08147812  
PATENT NO. 5766909  
GENERAL INFORMATION:  
APPLICANT: Xie, Qiao-wen  
APPLICANT: Nathan, Carl F.  
APPLICANT: Mumford, Richard A.  
APPLICANT: Calaycay, Jimmy Ramos  
TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Merck & Co., Inc.  
STREET: 126 East Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh Centris650  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/147,812  
FILING DATE: No. 5766909 Available  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/841,641  
FILING DATE: 02-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Wallen, John W III  
REGISTRATION NUMBER: 35,403  
REFERENCE/DOCKET NUMBER: 186581A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3905  
TELEFAX: (908) 594-4720  
TELEX: 138825  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1144 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-147-812-5

Query Match 96.1%; Score 99; DB 1; Length 1144;  
Best Local Similarity 94.4%; Pred. No. 2.2e-08;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVPFRSFQOQLHDSQH 18  
|||

Db 979 GIAPFRSFQOQLHDSQH 996

RESULT 7  
US-08-319-866-12  
SEQUENCE 12, Application US/08319866  
PATENT NO. 5929223  
GENERAL INFORMATION:  
APPLICANT: Tully, Timothy P.  
APPLICANT: Yin, Jerry C.  
APPLICANT: Regulski, Michael  
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES

```

Best Local Similarity 94.4%; Pred. No. 2.2e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVPFRSEWQRLHDSQH 18
   ||| ||||| ||||| |||
Db 979 GIAPFRSEWQRLHDSQH 996

RESULT 9
US-09-123-624-2
; Sequence 2, Application US/09123624
; Patent No. 6149936
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Jurgen
; APPLICANT: GODECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 511169-2004
; CURRENT APPLICATION NUMBER: US/09/123,624
; CURRENT FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 08/553,503
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: 4411402.8
; PRIOR FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-123-624-2

Query Match 96.1%; Score 99; DB 4; Length 1144;
Best Local Similarity 94.4%; Pred. No. 2.2e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 GIVFRSFQQRLHDSQH 18  
 II IIIIIIIIIIIII  
 Db 979 GIAPERSFQQRLHDSQH 996

GENERAL INFORMATION:  
APPLICANT: Thigpen, Anice  
APPLICANT: Hohmeier, Hans-Ewald  
APPLICANT: Newgard, Christopher B.  
APPLICANT: Unger, Roger H.  
APPLICANT: Shimabukuro, Michio  
APPLICANT: Chen, Guaxun  
APPLICANT: Rhodes, Christopher J.  
APPLICANT: Hugli, Sigrun R.  
APPLICANT: Cousin, Sharon  
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
TO NO-MEDIATED CYTOTOXICITY  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/125,109

;; FILING DATE: 30-JUL-1998  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 60/055,092  
;; FILING DATE: 30-JUL-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US Unknown  
;; FILING DATE: 03-MAR-1998  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McMillian, Nabeela R.  
;; REGISTRATION NUMBER: P-43,363  
;; REFERENCE/DOCKET NUMBER: UTSD:560  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (512) 418-3000  
;; TELEFAX: (512) 474-7577  
;; INFORMATION FOR SEQ ID NO: 12:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1146 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-126-109-12

Query Match 96.1%; Score 99; DB 4; Length 1146;  
Best Local Similarity 94.4%; Pred. No. 2.2e-08;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVPFRSFQOQLHDSQH 18  
|| |||||  
DB 985 GIAPFRSFQOQLHDSQH 1002

RESULT 11  
US-07-642-002-2  
; Sequence 2, Application US/07642002  
; Patent No. 5288465  
; GENERAL INFORMATION:  
; APPLICANT: Bredt, David S.  
; APPLICANT: Hwang, Paul M.  
; APPLICANT: Reed, Randall  
; APPLICANT: Snyder, Solomon H.  
; TITLE OF INVENTION: Purification and Molecular Cloning of Nitric  
; TITLE OF INVENTION: Oxide Synthase  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner, Birch, McKie & Beckett  
; STREET: One Thomas Circle, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/642,002  
; FILING DATE: 19910118  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 1107.033576  
; TELEPHONE: (202) 296-5500  
; TELEFAX: (202) 296-7830  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1429 amino acids  
; TYPE: AMINO ACID

;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-07-642-002-2

Query Match 75.7%; Score 78; DB 1; Length 1429;  
Best Local Similarity 77.8%; Pred. No. 8.3e-05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIVPFRSFQOQLHDSQH 18  
|| |||||  
DB 1252 GIAPFRSFQOQLHDSQH 1269

RESULT 12  
US-08-365-486A-13  
; Sequence 13, Application US/08365486A  
; Patent No. 5834306  
; GENERAL INFORMATION:  
; APPLICANT: Webster, Keith A.  
; APPLICANT: Bishopric, Nanette H.  
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
; TITLE OF INVENTION: Therapeutic Constructs  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/365,486A  
; FILING DATE: 23-DEC-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615  
; REFERENCE/DOCKET NUMBER: 8255-0018  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1429 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-365-486A-13

Query Match 75.7%; Score 78; DB 2; Length 1429;  
Best Local Similarity 77.8%; Pred. No. 8.3e-05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIVPFRSFQOQLHDSQH 18  
|| |||||  
DB 1252 GIAPFRSFQOQLHDSQH 1269

RESULT 13  
US-08-319-866-11  
; Sequence 11, Application US/08319866  
; Patent No. 5929223  
; GENERAL INFORMATION:  
; APPLICANT: Tully, Timothy P.  
; APPLICANT: Yin, Jerry C.  
; APPLICANT: Regulski, Michael

RESULT 14  
US-08-880-342-13  
; Sequence 13, Application US/08880342  
; Patent No. 6216179  
; GENERAL INFORMATION:  
; APPLICANT: Webster, Keith A.  
; APPLICANT: Bishopric, Nanette H.  
; APPLICANT: Murphy, Brian  
; APPLICANT: Laderoute, Keith R.  
; APPLICANT: Green, Christopher J.  
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
; TITLE OF INVENTION: Therapeutic Constructs  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version 1.25

Patent No. 5908/36

GENERAL INFORMATION:

APPLICANT: Snyder, Solomon H.

APPLICANT: Jaffrey, Samie R.

TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric

TITLE OF INVENTION: Oxide Synthase

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff

STREET: 1001 G Street, N.W.

CITY: Washington, D.C.

COUNTRY: U.S.A.

ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/705,625

FILING DATE: 30-AUG-1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.57071

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1430 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-705-625-4

Query Match 75.7%; Score 78; DB 2; Length 1430;  
Best Local Similarity 77.8%; Pred. No. 8.3e-05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIVPFRSFQQRLHDSQH 18  
|| ||||| || ||  
Db 1252 GIAPFRSFQQRQFDIQH 1269

Search completed: September 10, 2001, 14:01:55  
Job time: 224 sec

**This Page Blank (uspto)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 13:57:36 ; Search time 67.08 Seconds  
(without alignments)  
16.268 Million cell updates/sec

Title: US-08-833-506C-25

Perfect score: 103

Sequence: 1 GIVPFRSFQORLHDSQH 18

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

```

1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	103	100.0	18	AAW81241	Human iNOS peptide
2	103	100.0	18	AAW81186	Human iNOS (985-10
3	103	100.0	18	AAW81275	Human iNOS peptide
4	103	100.0	18	AAW81202	Human iNOS peptide
5	103	100.0	18	AAW81203	Human iNOS peptide
6	103	100.0	1153	AAW5764	Sequence encoded b
7	103	100.0	1153	AAW88464	Hepatocyte inducib
8	103	100.0	1153	AAW31724	Amino acid sequenc
9	103	100.0	1153	AAW66724	Human inducible ni
10	99	96.1	18	AAW81187	Mouse iNOS (978-99
11	99	96.1	18	AAW81188	Rat iNOS (982-998)

12	99	96.1	1144	16	AAW77360	Inducible nitrogen
13	99	96.1	1144	19	AAW51246	Inducible nitric o
14	99	96.1	1146	20	AAW96322	Inducible nitric o
15	99	96.1	1147	17	AAW02571	Rat inducible nitr
16	99	96.1	1153	15	AAW63206	Nitric-oxide-synth
17	99	96.1	1153	19	AAW36113	Human inducible ni
18	99	86.4	15	19	AAW81244	Human iNOS peptide
19	89	86.4	15	19	AAW81304	Human iNOS peptide
20	86	83.5	15	19	AAW81308	Human iNOS peptide
21	86	83.5	15	19	AAW81248	Human iNOS peptide
22	78	75.7	18	19	AAW81242	Human nNOS peptide
23	78	75.7	18	19	AAW81189	Human nNOS (1256-1
24	78	75.7	18	19	AAW81323	Human iNOS peptide
25	78	75.7	1429	14	AAW44489	Sequence of all or
26	78	75.7	1430	19	AAW56786	Rat neuronal nitri
27	78	75.7	1430	20	AAW28475	Rat neuronal nitri
28	78	75.7	1433	16	AAW77362	Neuronal nitrogen
29	78	75.7	1433	22	AAW31725	Amino acid sequenc
30	78	75.7	1433	22	AAW66725	Human nitric oxide
31	78	75.7	1463	18	AAW35566	Rat penile neurona
32	78	75.7	1554	20	AAW28476	Human neuronal nit
33	75	72.8	15	19	AAW81243	Human eNOS peptide
34	75	72.8	15	19	AAW81324	Human iNOS peptide
35	75	72.8	18	19	AAW81190	Human eNOS (1017-1
36	75	72.8	18	19	AAW81191	Bovine eNOS (1019-
37	75	72.8	1203	14	AAW41668	Human endothelial
38	75	72.8	1203	19	AAW57315	Human endothelial
39	75	72.8	1203	22	AAW31726	Amino acid sequenc
40	75	72.8	1203	22	AAW66726	Human nitric oxide
41	75	72.8	1205	16	AAW77363	Endothelial nitrog
42	75	72.8	1205	17	AAW93930	Bovine endothelial
43	71	68.9	12	19	AAW81245	Human iNOS peptide
44	71	68.9	12	19	AAW81305	Human iNOS peptide
45	68	66.0	12	19	AAW81309	Human iNOS peptide

#### ALIGNMENTS

RESULT	1
AAW81241	
ID	AAW81241 standard; peptide; 18 AA.
XX	
AC	AAW81241;
DT	30-APR-1999 (first entry)
XX	
DE	Human iNOS peptide fragment PS-5183.
XX	
KW	Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW	monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW	myocardial infarction; tissue rejection; transplantation; psoriasis;
KW	autoimmune disease; multiple sclerosis.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Modified-site 18
FT	Location/Qualifiers
XX	/note= "His residue amidated"
PN	WO9845710-A1.
XX	
PD	15-OCT-1998.
XX	
PF	11-APR-1997; 97WO-US06500.
XX	
PR	07-APR-1997; 97US-6667777.
XX	
PA	(WEBB/) WEBBER R.
XX	
PI	Webber R;
XX	
PI	WPI; 1998-594495/50.
DR	

```

XX Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
XX Example 4; Page 37; 93pp; English.
XX This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide fragment from human iNOS which is used in the method
XX of the invention.
XX Sequence 18 AA;
SQ
Query Match 100.0%; Score 103; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIVPFRSEWQRLHDSQH 18
DB 1 givprfstwqgrlhdsqh 18
|||||
RESULT 2
AAW81186
ID AAW81186 standard; peptide; 18 AA.
XX AC AAW81186;
XX 30-APR-1999 (first entry)
XX Human iNOS (985-1002) peptide fragment.
XX Inducible nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
XX OS Homo sapiens.
XX WO9845710-A1.
XX 15-OCT-1998.
XX 11-APR-1997; 97WO-US06500.
XX 07-APR-1997; 97US-6667777.
XX (WEBB/) WEBBER R.
XX Webber R;
XX WPI; 1998-594495/50.
XX Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
XX Disclosure; Page 21; 93pp; English.
XX This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
XX tissues for various pathophysiological conditions such as sepsis, septic
XX shock, myocardial infarction, rejection of tissue in organs following
XX transplantation, monitoring "flare ups" in certain autoimmune diseases
XX such as lupus, psoriasis, and multiple sclerosis. This sequence
XX represents a peptide from human iNOS which is used in the method of the
XX invention.
XX Sequence 18 AA;
SQ
Query Match 100.0%; Score 103; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIVPFRSEWQRLHDSQH 18
DB 1 givprfstwqgrlhdsqh 18
|||||
RESULT 3
AAW81275
ID AAW81275 standard; peptide; 18 AA.
XX AC AAW81275;
XX 30-APR-1999 (first entry)
XX Human iNOS peptide fragment #1.
XX Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
XX OS Homo sapiens.
XX WO9845710-A1.
XX 15-OCT-1998.
XX 11-APR-1997; 97WO-US06500.
XX 07-APR-1997; 97US-6667777.
XX (WEBB/) WEBBER R.
XX Webber R;
XX WPI; 1998-594495/50.
XX Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
XX Disclosure; Fig 1; 93pp; English.
XX This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention.
XX Sequence 18 AA;
SQ
Query Match 100.0%; Score 103; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIVPFRSEWQRLHDSQH 18
DB 1 givprfstwqgrlhdsqh 18
|||||

```

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVPFRSFQQRLHDSQH 18  
 |||||  
 Db 1 givpfrsfwqgrlhdsqh 18

## RESULT 4

AAW81202  
 ID AAW81202 standard; peptide; 18 AA.

XX AC

XX AAW81202;

DT 30-APR-1999 (first entry)

XX Human INOS peptide fragment capable of binding Mab 1E8-B8.

XX Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
 KW autoimmune disease; multiple sclerosis; Mab.

XX Homo sapiens.

XX WO9845710-A1.

XX 15-OCT-1998.

XX 11-APR-1997; 97WO-US06500.

XX 07-APR-1997; 97US-6667777.

XX (WEBB/) WEBBER R.

XX Webber R;

XX WPI; 1998-594495/50.

XX Detection of human inducible nitric oxide synthase - using an  
 PT immunoassay in which a sample is contacted with a specific binding  
 PT entity reactive with human iNOS or mimics.

XX Example 3; Page 32; 93pp; English.

XX This invention describes an immunoassay method where a sample with a  
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
 CC to detect the presence of human iNOS protein in the sample. The method  
 CC can be used for the detection and quantitation of human iNOS in cells and  
 CC tissues for various pathophysiological conditions such as sepsis, septic  
 CC shock, myocardial infarction, rejection of tissue in organs following  
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
 CC represents a peptide from human iNOS which is used in the method of the  
 CC invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 103; DB 19; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4e-10; Mismatches 0; Gaps 0;  
 Matches 18; Conservative 0; Indels 0;

QY 1 GIVPFRSFQQRLHDSQH 18  
 |||||  
 Db 1 givpfrsfwqgrlhdsqh 18

## RESULT 5

AAW81203  
 ID AAW81203 standard; peptide; 18 AA.

XX AC

XX AAW81203;

XX

DT 30-APR-1999 (first entry)

XX Human INOS peptide fragment capable of binding Mab 2A12-A4.

XX Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
 KW autoimmune disease; multiple sclerosis; Mab.

XX Homo sapiens.

XX WO9845710-A1.

XX 15-OCT-1998.

XX 11-APR-1997; 97WO-US06500.

XX 07-APR-1997; 97US-6667777.

XX (WEBB/) WEBBER R.

XX Webber R;

XX WPI; 1998-594495/50.

XX Detection of human inducible nitric oxide synthase - using an  
 PT immunoassay in which a sample is contacted with a specific binding  
 PT entity reactive with human iNOS or mimics.

XX Example 3; Page 32; 93pp; English.

XX This invention describes an immunoassay method where a sample with a  
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
 CC to detect the presence of human iNOS protein in the sample. The method  
 CC can be used for the detection and quantitation of human iNOS in cells and  
 CC tissues for various pathophysiological conditions such as sepsis, septic  
 CC shock, myocardial infarction, rejection of tissue in organs following  
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
 CC represents a peptide from human iNOS which is used in the method of the  
 CC invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 103; DB 19; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4e-10; Mismatches 0; Gaps 0;  
 Matches 18; Conservative 0; Indels 0;

QY 1 GIVPFRSFQQRLHDSQH 18  
 |||||  
 Db 1 givpfrsfwqgrlhdsqh 18

## RESULT 6

AAW5764  
 ID AAR55764 standard; Protein; 1153 AA.

XX AC

XX AAR55764;

XX 28-DEC-1994 (first entry)

XX Sequence encoded by the cDNA clone for human hepatocyte inducible  
 DE nitric oxide synthase.

XX Nitric oxide synthase; hepatocyte; hypotensive shock; therapy.

XX Homo sapiens.

XX WO9412645-A.

XX

```

PD 09-JUN-1994.
XX
XX
XX 23-NOV-1993; 93WO-US11401.
XX
XX 25-NOV-1992; 92US-0981344.
XX
XX (UYPI-) UNIV PITTSBURGH.
XX
XX Billiar TR, Geller DA, Nussler AK, Simmons RL;
XX
XX WPI; 1994-200273/24.
XX
XX N-PSDB; AAQ66914.
XX
XX cDNA clone encoding human inducible nitric oxide synthase - used
XX to prevent the hypotensive shock seen with sepsis.
XX
XX Disclosure; Fig 1; 53pp; English.
XX
XX AAQ66914 is from human hepatocyte inducible nitric oxide synthase cDNA
XX clone PHINOS from lambda Zap II cDNA library. The original source
XX was induced human hepatocyte RNA. HINOS cDNA plasmid is pref.
XX transformed in E. coli SOLR (ATCC 69126). The inventors claim a
XX clone with the cDNA sequence in AAQ66914 and a cDNA clone which
XX encodes AAR5764. The cloning and expression of a human tissue nitric
XX oxide synthase cDNA provides a source of the enzyme for therapeutic
XX purposes, for example to prevent the hypotensive shock seen with
XX sepsis.
XX
XX SQ Sequence 1153 AA;

Query Match 100.0%; Score 103; DB 15; Length 1153;
Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVPFRSEWQRLHDSQH 18
Db 985 givpfrsfwqrlhdsqh 1002
|||||
RESULT 7
AAR88464
ID AAR88464 standard; Protein; 1153 AA.
XX
XX AC AAR88464;
XX
XX DT 13-MAY-1996 (first entry)
XX
XX DE Hepatocyte inducible nitric oxide synthase.
XX
XX KW Inducible nitric oxide synthase; INOS; hepatocyte; gene therapy;
XX
XX KW vascular occlusive disease; cancer; infection.
XX
XX OS Homo sapiens.
XX
XX PN WO9600006-A1.
XX
XX PD 04-JAN-1996.
XX
XX PF 20-JUN-1995; 95WO-US07849.
XX
XX PR 24-JUN-1994; 94US-0265046.
XX
XX PA (UYPI-) UNIV PITTSBURGH.
XX
XX PI Billiar TR, Geller DA, Nussler AK, Simmons RL, Tzeng E;
XX
XX WPI; 1996-068641/07.
XX
XX N-PSDB; AAT10115.
XX
XX Inducible nitric oxide synthase gene - useful in gene therapy to
XX treat, e.g. vascular occlusive disease and cancer
XX

PS Disclosure; Page 54-58; 91pp; English.
XX
XX CC An inducible nitric oxide synthase (INOS - AAR88464) is the product
XX of a cDNA clone (AAT10115) derived from human hepatocytes induced
XX for INOS biosynthesis. The INOS can be obtd. by expression of
XX the cDNA e.g. in mammalian host cells and is used in the
XX development of selective inhibitors of NOS or to treat diseases
XX affected by nitric oxide.
XX
XX SQ Sequence 1153 AA;

Query Match 100.0%; Score 103; DB 17; Length 1153;
Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVPFRSEWQRLHDSQH 18
Db 985 givpfrsfwqrlhdsqh 1002
|||||
RESULT 8
AAB31724
ID AAB31724 standard; Protein; 1153 AA.
XX
XX AC AAB31724;
XX
XX DT 30-APR-2001 (first entry)
XX
XX DE Amino acid sequence of a human inducible nitric oxide synthase (NOS).
XX
XX KW Gene therapy; angiogenesis; nucleic acid delivery; arteriosclerosis;
XX nitric oxide synthase; NOS; endothelial dysfunction.
XX
XX OS Homo sapiens.
XX
XX PN WO200103728-A2.
XX
XX PD 18-JAN-2001.
XX
XX PF 07-JUL-2000; 2000WO-NL00482.
XX
XX PR 09-JUL-1999; 99EP-0202263.
XX
XX PR 09-JUL-1999; 99US-0143101.
XX
XX PA (INTR-) INTROGENE BV.
XX
XX PI Vogels R, Verlinden SFF;
XX
XX DR WPI; 2001-123142/13.
XX
XX PT Nucleic acid delivery vehicle comprising a nucleic acid encoding nitric
XX oxide synthase, used for isolated tissue perfusion treatment to enhance
XX and induce angiogenesis -
XX
XX PS Disclosure; Fig 6; 37pp; English.
XX
XX CC The specification describes a method for gene therapy for enhancing
XX and inducing angiogenesis. The method uses a nucleic acid delivery
XX vehicle, which comprises a nucleic acid encoding nitric oxide synthase
XX (NOS). The delivery vehicle is used for the manufacture of a
XX pharmaceutical composition for isolated tissue perfusion treatment.
XX The method is useful for enhancing and/or inducing angiogenesis in
XX patients with endothelial dysfunctions, in particular arteriosclerosis.
XX The present sequence represents an inducible NOS.
XX
XX SQ Sequence 1153 AA;

Query Match 100.0%; Score 103; DB 22; Length 1153;
Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GIVPFRFWOORLHDSQH 18  
 Db 985 givpfrfwqqrllhdsqh 1002

## RESULT 9

AAW866724  
 ID AAB66724 standard; protein; 1153 AA.

XX AC AAB66724;  
 XX 09-APR-2001 (first entry)  
 XX Human Inducible nitric oxide synthase.  
 XX Nitric oxide synthase; NOS; angiogenesis; gene therapy.  
 XX Homo sapiens.  
 XX EP1067190-A1.  
 XX 10-JAN-2001.  
 XX 09-JUL-1999; 99EP-0202263.  
 XX 09-JUL-1999; 99EP-0202263.  
 XX (INTR-) INTROGENE BV.  
 XX Vogels R, Verlinden S;  
 XX WPI; 2001-125729/14.  
 XX Use of a nucleic acid delivery vehicle comprising a nucleic acid  
 PT encoding nitric oxide synthase, especially useful in gene therapy for  
 PT enhancing and/or inducing angiogenesis and treating atherosclerosis -  
 XX Examples; Page 14-18; 39pp; English.  
 XX The present invention relates to use of a nucleic acid delivery  
 CC vehicle comprising a nucleic acid encoding nitric oxide synthase  
 CC (NOS) activity for the manufacture of a composition for essentially  
 CC isolated tissue perfusion treatment to enhance and/or induce  
 CC angiogenesis. The nucleic acid delivery vehicle is particularly  
 CC useful in gene therapy for the treatment of atherosclerosis.  
 XX SQ Sequence 1153 AA;

Query Match 100.0%; Score 103; DB 22; Length 1153;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVPFRFWOORLHDSQH 18  
 Db 985 givpfrfwqqrllhdsqh 1002

## RESULT 10

AAW81187  
 ID AAW81187 standard; peptide; 18 AA.

XX AC AAW81187;  
 XX 30-APR-1999 (first entry)  
 XX Mouse iNOS (978-995) peptide fragment.  
 XX Inducible nitric oxide synthase; iNOS; murine; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
 KW autoimmune disease; multiple sclerosis.  
 XX

OS Mus sp.  
 XX WO9845710-A1.  
 XX 15-OCT-1998.  
 XX 11-APR-1997; 97WO-US06500.  
 XX 07-APR-1997; 97US-6667777.  
 XX (WEBB/) WEBBER R.  
 XX Webber R;  
 XX WPI; 1998-594495/50.  
 XX Detection of human inducible nitric oxide synthase - using an  
 PT immunoassay in which a sample is contacted with a specific binding  
 PT entity reactive with human iNOS or mimics.  
 XX Disclosure; Page 21; 93pp; English.  
 XX This invention describes an immunoassay method where a sample with a  
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
 CC to detect the presence of human iNOS protein in the sample. The method  
 CC can be used for the detection and quantitation of human iNOS in cells and  
 CC tissues for various pathological conditions such as sepsis, septic  
 CC shock, myocardial infarction, rejection of tissue in organs following  
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
 CC represents a peptide fragment from mouse iNOS which is used in the method  
 CC of the invention.  
 XX SQ Sequence 18 AA;

Query Match 96.1%; Score 99; DB 19; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-09;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVPFRFWOORLHDSQH 18  
 Db 1 givpfrfwqqrllhdsqh 18

## RESULT 11

AAW81188  
 ID AAW81188 standard; peptide; 18 AA.

XX AC AAW81188;  
 XX 30-APR-1999 (first entry)  
 XX Rat iNOS (982-998) peptide fragment.  
 XX Inducible nitric oxide synthase; iNOS; rat; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
 KW autoimmune disease; multiple sclerosis.  
 XX OS Rattus sp.  
 XX WO9845710-A1.  
 XX 15-OCT-1998.  
 XX 11-APR-1997; 97WO-US06500.  
 XX 07-APR-1997; 97US-6667777.  
 XX (WEBB/) WEBBER R.  
 XX

PI Webber R;  
 XX WPI; 1998-594495/50.  
 XX  
 XX Detection of human Inducible nitric oxide synthase - using an  
 PT immunoassay in which a sample is contacted with a specific binding  
 PT entity reactive with human iNOS or mimics.  
 XX  
 XX  
 PS Disclosure; Page 21; 93pp; English.  
 XX  
 XX This invention describes an immunoassay method where a sample with a  
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
 CC to detect the presence of human iNOS protein in the sample. The method  
 CC can be used for the detection and quantitation of human iNOS in cells and  
 CC tissues for various pathophysiological conditions such as sepsis, septic  
 CC shock, myocardial infarction, rejection of tissue in organs following  
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
 CC represents a peptide fragment from rat iNOS which is used in the method  
 CC of the invention.  
 XX  
 XX Sequence 18 AA;  
 SQ  
 Query Match 96.1%; Score 99; DB 19; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-09;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GIVPFRSFQQRRLHDSQH 18  
 DB 1 giapfrsfwqqrllhdsqh 18  
 RESULT 12  
 AAR77360  
 ID AAR77360 standard; Protein; 1144 AA.  
 XX  
 AC AAR77360;  
 XX  
 XX 10-MAY-1996 (first entry)  
 DT  
 DE Inducible nitrogen monoxide synthase.  
 DE nitrogen monoxide synthase; inducible; treatment; prevention;  
 KW vascular disease; restenosis.  
 KW  
 XX Mus musculus.  
 XX  
 XX DE4411402-A1.  
 PN  
 XX  
 PD 05-OCT-1995.  
 XX  
 XX 31-MAR-1994; 94DE-4411402.  
 PF  
 XX 31-MAR-1994; 94DE-4411402.  
 PR  
 XX (SCHR/) SCHRADER J.  
 PA  
 XX Goedecke A, Schrader J;  
 PI WPI; 1995-345550/45.  
 DR N-PSDB; AAQ94252.  
 DR  
 XX  
 XX Eukaryotic expression vector for nitrogen-mon:oxide synthase gene -  
 PT useful in the treatment and prevention of diseases of blood vessels  
 PT by gene therapy  
 PT  
 XX Claim 5; Fig 1; 28pp; German.  
 PS  
 XX Inducible nitrogen monoxide synthase (iNOS) was isolated from mice, and  
 CC is encoded by AAQ94252. iNOS is homodimer with a mol. wt. of 130 kDa  
 CC per subunit. The activity of iNOS is independent of calmodulin and

CC cellular calcium levels. Vectors contg. the DNA are used in the  
 CC treatment or prevention of vascular diseases, high blood pressure,  
 CC arteriosclerosis, stenosis or restenosis of blood vessels, esp. coronary  
 CC vessels after percutane transluminal coronary angioplasty. See AAR77363  
 CC and AAR77362 for endothelial and brain-derived NOS.  
 XX  
 XX Sequence 1144 AA;  
 SQ

Query Match 96.1%; Score 99; DB 16; Length 1144;  
 Best Local Similarity 94.4%; Pred. No. 1.2e-07;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVPFRSFQQRRLHDSQH 18  
 DB 979 giapfrsfwqqrllhdsqh 996

## RESULT 13

AAR51246  
 ID AAR51246 standard; Protein; 1144 AA.

XX  
 AC AAR51246;

XX 12-AUG-1998 (first entry)

XX Inducible nitric oxide synthase, long isoform.

DE Inducible nitric oxide synthase; iNOS; recombinant protein;  
 KW cDNA library; isoform.

XX Mus sp.

XX US5766909-A.

PN 16-JUN-1998.

XX 05-NOV-1993; 93US-0841641.

XX 05-NOV-1993; 93US-0147812.

PR 04-FEB-1992; 92US-0841641.

XX (MERI ) MERCK & CO INC.

XX Calatcay JR, Mumford RA, Nathan CF, Xie Q;

XX WPI; 1998-361696/31.

DR N-PSDB; AAV07247.

XX DNA encoding inducible nitric oxide synthase proteins - useful for  
 PT producing recombinant proteins

XX Claim 1; Columns 25-32; 39pp; English.

XX The invention relates to two DNA molecules encoding inducible nitric  
 CC oxide synthase (iNOS) proteins, where the DNA molecules comprise defined  
 CC sequences of 4041 and 4165 base pairs given in the specification and the  
 CC proteins have 1144 amino acids. Also claimed are expression vectors and  
 CC containing the DNA molecules, and recombinant host cells containing the  
 CC vectors. The DNA molecules are useful for producing the recombinant  
 CC proteins. The present sequence represents inducible nitric oxide, long  
 CC isoform.

XX Sequence 1144 AA;  
 SQ

Query Match 96.1%; Score 99; DB 19; Length 1144;  
 Best Local Similarity 94.4%; Pred. No. 1.2e-07;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVPFRSFQQRRLHDSQH 18

DB 979 giapfrsfwqqrllhdsqh 996

RESULT 14  
AAW96322  
ID AAW96322 standard; Protein; 1146 AA.  
XX AC AAW96322;  
XX DT 28-JUN-1999 (first entry)  
XX DE Inducible nitric oxide synthase.  
XX KW Manganese containing superoxide dismutase; MnSOD; IDDM;  
XX KW diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell;  
XX KW fatty acid; lipotoxic; cytotoxic; cytokine; osteoporosis;  
XX KW inflammatory disease; autoimmune disease; neurodegenerative disease.  
XX OS Homo sapiens.  
XX PN WO9906059-A2.  
XX PD 11-FEB-1999.  
XX PF 30-JUL-1998; 98WO-US15781.  
XX PR 03-MAR-1998; 98US-0055092.  
XX PR 30-JUL-1997; 97US-0055092.  
XX PA (BETA-) BETAGENE INC.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX PI Clark SA, Hohmeier H, Koyama K, Lee Y, Newgard CB;  
XX PI Ohneda M, Shlmabukurum, Thidpen A, Unger RH;  
XX DR WPI; 1999-153448/13.  
XX DR N-PSDB; AAX08434.  
XX PT Protection of mammalian cells against immunotoxicity or lipotoxicity  
XX PT - used for treating, e.g. diabetes, obesity, wasting syndromes,  
XX PT osteoporosis, inflammatory diseases, autoimmune diseases or  
XX PT neurodegenerative diseases  
XX PS Disclosure; Page 247-251; 253pp; English.  
XX CC Inhibition of cytokine mediated immunotoxicity of cells can be  
XX CC achieved by blocking free radical production or the accumulation of  
XX CC free radicals in that cell. Treatment of insulin dependent diabetes  
XX CC mellitus (IDDM) can be achieved by blocking nitric oxide (NO)  
XX CC production in a pancreatic beta cell and by providing a composition  
XX CC comprising an agent that reduces levels of fatty acids in the cells  
XX CC and protects beta-cells of the subject against lipid-mediated cell  
XX CC death. Cells can also be protected against nitric oxide mediated  
XX CC cytotoxicity by introducing into the cell an antioxidant agent.  
XX CC The methods can be used for protecting cells against immunotoxicity  
XX CC mediated by, e. g. IL-1 beta, IL-1 alpha, gamma IFN, TNF alpha, TNF  
XX CC beta, IL-8, IL-2, IL-6, IL-3, IL-5, IL-7, IL-9, IL-14, IL-17,  
XX CC granulocyte-macrophage colony stimulating factor or monocyte  
XX CC chemoattractant protein-1. The methods can be used for the treatment  
XX CC of e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity,  
XX CC wasting syndromes, short stature, osteoporosis, inflammatory  
XX CC diseases, autoimmune diseases, or neurodegenerative diseases.  
XX SQ Sequence 1146 AA;

Query Match 96.1%; Score 99; DB 20; Length 1146;  
Best Local Similarity 94.4%; Pred. No. 1.2e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVPFRSFQQRLHDSOH 18  
||| ||||| ||||| |||||

Db 985 giapfrsfwqqlhdsq 1002

RESULT 15  
AAW02571  
ID AAW02571 standard; Protein; 1147 AA.  
XX AC AAW02571;  
XX DT 23-OCT-1996 (first entry)  
XX DE Rat inducible nitric oxide synthase.  
XX KW Inducible nitric oxide synthase; iNOS; erectile dysfunction;  
XX KW gene therapy; penile smooth muscle cell; PSMC; impotence.  
XX OS Rattus sp.  
XX FH Key Location/Qualifiers  
XX FT Misc-difference 270 /note= "in vascular iNOS, amino acid 270 is Pro"  
XX FT Misc-difference 349 /note= "in vascular iNOS, amino acid 349 is Ala  
XX FT /note= "in vascular iNOS, amino acid 349 is Ala  
XX FT Misc-difference 591 /note= "in vascular iNOS, amino acid 591 is Val"  
XX FT Misc-difference 721 /note= "in vascular iNOS, amino acid 721 is Pro  
XX FT /note= "in vascular iNOS, amino acid 721 is Pro  
XX FT Misc-difference 741 /note= "in vascular iNOS, amino acid 741 is Pro  
XX FT Or Leu"  
XX FT Misc-difference 1034 /note= "in vascular iNOS, amino acid 1084 is Ile  
XX FT Or Met"  
XX PN WO9614748-A1.  
XX PD 23-MAY-1996.  
XX PF 09-NOV-1995; 95WO-US14588.  
XX PR 10-NOV-1994; 94US-0337357.  
XX PA (NIRE-) NIREC INC..  
XX PI Gonzalez-Cadavid NF, Rajfer J;  
XX WPI: 1996-277317/28.  
XX DR N-PSDB; AAT32655.  
XX PT Treating erectile dysfunction by increasing level of nitric oxide  
XX PT synthase - in penile tissue, e.g. by admin. of cDNA or enzyme  
XX PT inducers, also new DNA, vectors, transformed cells and enzymes  
XX PS Claim 29; Page 37-38; 68pp; English.  
XX CC The amino acid sequence (AAW02571) of rat inducible nitric oxide  
XX CC synthase (iNOS) (AAW02571) was deduced from cDNA clones (see also  
XX CC AAT32655) obt'd. from rat penile smooth muscle cells (PSMC). 6  
XX CC Amino acid differences were found from vascular iNOS sequences.  
XX CC Recombinant iNOS or iNOS-expressing transformed PSMC cells can be  
XX CC used to ameliorate erectile vasculogenic dysfunction in the penis  
XX CC for the treatment of impotence (NO is the main mediator of erection).  
XX CC The transformed cells can be implanted directly into corpora  
XX CC cavernosa or retained in microcapsules, pellets, etc., allowing in  
XX CC vivo prodn. of NO.  
XX SQ Sequence 1147 AA;

Query Match 96.1%; Score 99; DB 17; Length 1147;  
Best Local Similarity 94.4%; Pred. No. 1.2e-07;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:11:11 ; Search time 72.54 Seconds  
(without alignments)  
32.830 Million cell updates/sec

Title: US-08-833-506C-26

Perfect score: 96

Sequence: 1 SPVTQDDLQYHNLKQON 18

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.16.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_unclassified.\*  
13: sp\_vertibrate.\*  
14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	96	100.0	1114	4	O94994 homo sapien
2	44.5	46.4	1154	6	O97604 canis famli
3	44	45.8	1268	5	O9V419 drosophila
4	44	45.8	1299	5	O9U5X0 drosophila
5	43	44.8	196	2	O9KJD8 lactococcus
6	43	44.8	300	2	O9XDM4 salmonella
7	43	44.8	447	10	O9LR71 arabidopsis
8	43	44.8	647	3	O99077 ustilago ho
9	43	44.8	850	4	O9Y5E0 homo sapien
10	43	44.8	856	5	O9V706 drosophila
11	43	44.8	936	4	O9V5H3 homo sapien
12	43	44.8	1032	3	O02932 saccharomyc
13	43	44.8	1801	5	O9NAI3 caenorhabdi
14	43	44.8	1840	11	O61818 mus musculu
15	42.5	44.3	1281	5	O97276 plasmodium
16	42	43.8	186	10	O9ZSP0 oryza sativ
17	42	43.8	264	2	O9KUD0 vibrio chol
18	42	43.8	387	5	O17845 caenorhabdi
19	42	43.8	395	5	O94181 caenorhabdi

20	42	43.8	597	2	O9K9C2	O9K9C2 bacillus ha
21	41.5	43.2	1147	11	O9R0W4	O9R0W4 rattus norv
22	41.5	43.2	1147	11	O9QW28	O9QW28 rattus sp.
23	41	42.7	166	13	O9DE41	O9de41 gallus gall
24	41	42.7	356	2	O9ZHK7	O9zhk7 pasteurella
25	41	42.7	387	5	O9CYV5	O9cyv5 drosophila
26	41	42.7	400	4	O15298	O15298 homo sapien
27	41	42.7	400	4	O9H2G9	O9h2g9 homo sapien
28	41	42.7	488	2	O9PHV0	O9phv0 campylobact
29	41	42.7	857	5	O9V6Z4	O9V6Z4 drosophila
30	41	42.7	962	10	O9LRX1	O9lrx1 arabidopsis
31	41	42.7	991	3	O12252	O12252 saccharomyc
32	41	42.7	1192	5	O96127	O96127 plasmodium
33	41	42.7	1302	5	O9VRW3	O9vrw3 drosophila
34	40	41.7	246	5	O9V4S4	O9v4s4 drosophila
35	40	41.7	348	4	O14025	O14025 homo sapien
36	40	41.7	350	4	P78391	P78391 homo sapien
37	40	41.7	397	8	O21164	O21164 fusarium ox
38	40	41.7	402	4	P78392	P78392 homo sapien
39	40	41.7	448	10	O9ZQZ7	O9zqz7 arabidopsis
40	40	41.7	527	8	O9XNK5	O9xnk5 fusarium ox
41	40	41.7	539	2	O9FC66	O9fc66 streptomyce
42	40	41.7	542	2	O34427	O34427 bacillus su
43	40	41.7	547	2	O9X3W6	O9x3w6 zymomonas m
44	40	41.7	637	4	O14024	O14024 homo sapien
45	40	41.7	648	4	O9YZH7	O9yzh7 homo sapien

## ALIGNMENTS

RESULT 1  
O94994  
ID O94994 PRELIMINARY; PRT; 1114 AA.  
AC O94994;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE INDUCIBLE NITRIC OXIDE SYNTHASE.  
GN INOS.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RA Ogawa Y., Nishijima S., Goto M., Ida M.;

RT "Cloning and characterization of a novel splice valiant of human  
RT inducible nitric oxide synthase."

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB022318; BAA37123.1; -

DR HSSP; P35228; 4NOS.

DR InterPro; IPR001094; -

DR InterPro; IPR001433; -

DR InterPro; IPR001709; -

DR InterPro; IPR003097; -

DR Pfam; PF00175; oxidored\_fad; 1.

DR Pfam; PF00667; FAD\_binding; 1.

DR PRINTS; PR00369; FLAVODOXIN.

DR PRINTS; PR00371; FPNCR.

SQ SEQUENCE 1114 AA; 126748 MW; C1F9624774435571 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 1114;

Best Local Similarity 100.0%; Pred. No. 6.3e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVTQDDLQYHNLKQON 18

Db 37 SPVTQDDLQYHNLKQON 54

RESULT 2

O97604  
 ID O97604 PRELIMINARY; PRT; 1154 AA.  
 AC O97604;  
 DT 01-MAY-1999 (TReMBLrel. 10, Created)  
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE INDUCIBLE NITRIC OXIDE SYNTHASE.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=AORTA;  
 RX MEDLINE=98431941; PubMed=9746458;  
 RA Wang X., McGregor C.G.A., Miller V.M.;  
 RT "Induction and cDNA sequence of inducible nitric oxide synthase from  
 canine aortic smooth muscle cells."  
 RL Am. J. Physiol. 275:H1122-H1129(1998).  
 DR EMBL; AF077821; AAC78630.1; -;  
 DR HSP; P29477; INOS.  
 DR InterPro; IPR001094; -;  
 DR InterPro; IPR001433; -;  
 DR InterPro; IPR001709; -;  
 DR InterPro; IPR003097; -;  
 DR Pfam; PF00175; oxidored\_fad; 1.  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 SQ SEQUENCE 1154 AA; 131709 MW; 42CD605E447254CB CRC64;  
  
 Query Match 46.4%; Score 44.5; DB 6; Length 1154;  
 Best Local Similarity 57.9%; Pred. No. 40;  
 Matches 11; Conservative 2; Mismatches 3; Indels 3; Gaps 1;  
  
 Qy 1 SPVTQDDL---QYHNLSKQ 16  
 ||||||| :||| |  
 Db 37 SPSTQDDLKNHKNHDSQ 55  
  
 RESULT 3  
 Q9V4I9  
 ID Q9V4I9 PRELIMINARY; PRT; 1268 AA.  
 AC Q9V4I9;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE CG11084 PROTEIN.  
 GN PK OR CG11084.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadelu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 CC Science 287:2185-2195(2000).  
 CC -1- SIMILARITY: CONTAINS LIM DOMAIN(S). THE LIM DOMAIN BINDS 2 ZINC  
 CC IONS  
 CC EMBL; AE003842; AAF59281.1; -;  
 DR HSP; P04006; LIML.  
 DR Flybase; FBgn0003090; pk.  
 DR InterPro; IPR000822; -;  
 DR InterPro; IPR001781; -;  
 DR Pfam; PF00412; LIM; 2.  
 DR PROSITE; PS00478; LIM\_DOMAIN\_1; 2.  
 DR PROSITE; PS00023; LIM\_DOMAIN\_2; 3.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2; UNKNOWN\_1.  
 DR SMART; SM00132; LIM; 1.  
 KW LIM motif; Metal-binding; Zinc.  
 SQ SEQUENCE 1268 AA; 137228 MW; AC4F9615A7C18C9E CRC64;  
  
 Query Match 45.8%; Score 44; DB 5; Length 1268;  
 Best Local Similarity 56.2%; Pred. No. 53;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
 Qy 2 PVTQDDLQYHNLSKQ 17  
 ||| ||| ||| |  
 Db 292 PLTAGDLQFLNLSLQ 307  
  
 RESULT 4  
 Q9U5X0  
 ID Q9U5X0 PRELIMINARY; PRT; 1299 AA.  
 AC Q9U5X0;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE PRICKLE SPLE ISOFORM.  
 GN PK OR CG11084.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ISOGENIC DP CN BW;  
 RX MEDLINE=99415814; PubMed=10485852;  
 RA Gubb D., Green C., Huen D., Coulson D., Johnson G., Tree D.,  
 RA Collier S., Roote J.;  
 RA "The balance between isoforms of the Prickle LIM domain protein is  
 RT critical for planar polarity in Drosophila imaginal discs."  
 RL Genes Dev. 13:2315-2327(1999).  
 RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=LT2;  
RX MEDLINE=94350831; PubMed=8071226;  
RA Chen P., Andersson D.I., Roth J.R.;  
RT "The control region of the pdu/cob regulon in Salmonella  
RL typhimurium.";  
RN J. Bacteriol. 176:5474-5482(1994).  
RP [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=LT2;  
RX MEDLINE=98012959; PubMed=9352910;  
RA Bobik T.A., Xu Y., Jeter R.M., Otto K.E., Roth J.R.;  
RT "Propanediol utilization genes (pdu) of Salmonella typhimurium: three  
RL genes for the propanediol dehydratase.";  
RN J. Bacteriol. 179:6633-6639(1997).  
RP [3]  
RN SEQUENCE FROM N.A.  
RC STRAIN=LT2;  
RX STRAIN=LT2;  
RA Bobik T.A., Xu Y., Jeter R.M., Otto K.E., Roth J.R.;  
RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RN SEQUENCE FROM N.A.  
RC STRAIN=LT2;  
RA Bobik T.A., Busch R.J., Havemann G.D., Williams D.S., Aldrich H.C.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF026270; AAD39022.1; -;  
DR InterPro; IPR000888; -;  
DR ProDom; PD001462; -; 1.  
SQ SEQUENCE 300 AA; 32786 MW; 18CB37B92A50856B CRC64;

Query Match 44.8%; Score 43; DB 2; Length 300;  
Best Local Similarity 52.9%; Pred. No. 18;  
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps

Oy 1 SPVTQDDLQYHNLSKQ 17  
||||| ||| :||  
Db 169 SPVTLRTQDYHRLPRQ 185

RESULT 7  
Q9LW71  
ID Q9LW71 PRELIMINARY; PRT; 447 AA.  
AC Q9LW71;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
F21B7.14.  
DE Arabidopsis thaliana (Mouse-ear cross).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
[1]  
RN SEQUENCE FROM N.A.  
RA Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,  
RA Shinn P., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,  
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,  
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsy N., Nguyen M.,  
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,  
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,  
RA Ecker J.R.;  
RT "Genomic sequence for Arabidopsis thaliana BAC F21B7 from chromosome  
RL 1.";  
RN Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RN SEQUENCE FROM N.A.  
RA Ecker J.R.;  
RT Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN SEQUENCE FROM N.A.  
RA Ecker J.R.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.



RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Flossler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasner K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Rhue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:  
 RA "The genome sequence of *Drosophila melanogaster*.";  
 RT Science 287:2185-2195(2000).  
 RL SGL; AF003815; AAF58260.1; -;  
 DR FlyBase; FBgn0033922; CG13942.  
 DR InterPro; IPR002965; -;  
 DR PRINTS; PR01217; PRICHTXTNSN.  
 DR PROSITE; PS00232; CADHERIN; 5.  
 SQ SEQUENCE 856 AA; 93777 MW; 3B6C3F80DFAE12B7 CRC64;

Query Match 44.8%; Score 43; DB 5; Length 856;  
 Best Local Similarity 61.5%; Pred. No. 53;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 QDDLOYHNLSKQ 17  
 |||||:|:|:|  
 DB 8 QDDLPNHNSSSQ 20

RESULT 11  
 QY5H3  
 ID QY5H3 PRELIMINARY; PRT; 936 AA.  
 AC QY5H3  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-NOV-2001 (TREMBlrel. 16, Last annotation update)  
 DE PROTOCADHERIN GAMMA A10.  
 GN PCDH-GAMMA-A10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=93308636; PubMed=10380929;  
 RA Wu Q., Maniatis T.;  
 RA "A striking organization of a large family of human neural cadherin-  
 RT like cell adhesion genes.";  
 RL Cell 97:779-790(1999).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: TO THE CADHERIN FAMILY.  
 DR EMBL; AF152319; RAD43713.1; -;  
 DR HSP; P15116; INCIJ.  
 DR InterPro; IPR002126; -;  
 DR Pfam; PF00028; cadherin. 6.  
 DR PRINTS; PR00205; CADHERIN.  
 DR PROSITE; PS00232; CADHERIN; 5.

DR SMART; SM00112; CA; 1.  
 SQ SEQUENCE 936 AA; 101445 MW; 5F614F1934D5DC61 CRC64;  
 Query Match 44.8%; Score 43; DB 4; Length 936;  
 Best Local Similarity 38.5%; Pred. No. 58;  
 Matches 10; Conservative 3; Mismatches 5; Indels 8; Gaps 1;  
 QY 1 SPVTQDD-----LQYHNLSKQ 18  
 |||||:|:|:|  
 DB 358 SPVTEDSPLGTVALNVHDLSEQN 383  
 RESULT 12  
 QY2932  
 ID QY2932 PRELIMINARY; PRT; 1032 AA.  
 AC QY2932;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE LPH2P.  
 GN LPH2W OR KAP120.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85054621; PubMed=6094498;  
 RA Sumrada R.A., Cooper T.G.;  
 RT "Nucleotide sequence of the *Saccharomyces cerevisiae* arginase gene  
 RT (CAR1) and its transcription under various physiological conditions.";  
 RL J. Bacteriol. 160:1078-1087(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90037050; PubMed=2681212;  
 RA Anderson M.S., Muehlbacher M., Street I.P., Proffitt J., Poulter C.D.;  
 RT "Isopentenyl diphosphate:dimethylallyl diphosphate isomerase. An  
 RT improved purification of the enzyme and isolation of the gene from  
 RT *Saccharomyces cerevisiae*.";  
 RL J. Biol. Chem. 264:19169-19175(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91312117; PubMed=1857205;  
 RA Jamieson D.J., Beggs J.D.;  
 RT "A suppressor of yeast spp81/decl mutations encodes a very similar  
 RT putative ATP-dependent RNA helicase.";  
 RL Mol. Microbiol. 5:805-812(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94131990; PubMed=8300560;  
 RA Zheng Y., Cerione R., Bender A.;  
 RT "Control of the yeast bud-site assembly GTPase Cdc42. Catalysis of  
 RT guanine nucleotide exchange by Cdc24 and stimulation of GTPase  
 RT activity by Bem3.";  
 RL J. Biol. Chem. 269:2369-2372(1994).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97313271; PubMed=9169875;  
 RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansoerge W.,  
 RA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,  
 RA Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,  
 RA Churche C., Coster F., Davis K., Davis R.W., Dietrich F.S.,  
 RA Delius H., DiPaolo T., Dubois E., Dusterhoft A., Duncan M., Floeth M.,  
 RA Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,  
 RA Heumann K., Hilbert H., Hillier L., Hunnicke-Smith S., Hyman R.,  
 RA Johnston M., Kallman S., Kleine K., Komp C., Kurdi O., Lashkari D.,  
 RA Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F.,  
 RA Mewes H.W., Mirtipati S., Moestl D., Muller-Auer S., Namath A.,  
 RA Nettwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M.,  
 RA Purnelle D., Schafer M., Scharfe M., Scherens B., Schramm S.,  
 RA Schroeder M., Sdicu A.M., Tettelin H., Urrestarazu L.A., Ushinsky S.,



Search completed: September 10, 2001, 14:11:12  
Job time: 591 sec

---

**This Page Blank (uspto)**



GenCore version 4.5

Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:09:51 ; Search time 23.82 Seconds  
(without alignments)  
25.886 Million cell updates/sec

Title: US-08-833-506C-26

Perfect score: 96

Sequence: 1 SPVTQDDLQYHNLSKQON 18

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	1153	1 NS2A_HUMAN	P35228 homo sapien
2	81	84.4	162	1 NOS2_MACMU	O46660 macaca mula
3	45	45.9	629	1 T3MH_HAEIN	P71366 haemophilus
4	45	46.9	705	1 YNP9_CAEEL	P34562 caenorhabdi
5	44	45.8	266	1 PANB_PSEFL	O92ep8 pseudomonas
6	43	44.8	288	1 YHCS_HAEIN	P43011 haemophilus
7	42	43.8	661	1 CAOL_CANTR	P08790 candida tro
8	41.5	43.2	497	1 MURE_BUCAI	P57316 buchnera ap
9	41.5	43.2	1147	1 NOS2_RAT	O06518 rattus norv
10	41.5	43.2	1147	1 NS2D_HUMAN	O60591 homo sapien
11	41	42.7	235	1 NCAP_HUNSH	P03513 bunyavirus
12	41	42.7	292	1 MURE_BUCAP	O85298 buchnera ap
13	41	42.7	606	1 RP3A_MOUSE	P47708 mus musculu
14	41	42.7	626	1 PC11_YEAST	P39081 saccharomyc
15	41	42.7	684	1 RP3A_RAT	P47709 rattus norv
16	41	42.7	1149	1 NOS2_CAVPO	O54705 cavia porce
17	41	42.7	1302	1 MDR5_DROME	O00748 drosophila
18	40	41.7	126	1 GP48_BFSP1	O48402 bacterioph
19	40	41.7	452	1 CLG1_YEAST	P35190 saccharomyc
20	40	41.7	597	1 ZF37_HUMAN	O9V6q3 homo sapien
21	40	41.7	640	1 MYB_HUMAN	P10242 homo sapien
22	40	41.7	740	1 PEG1_PIG	O95242 sus scrofa
23	40	41.7	1009	1 CHS2_CANAL	P30572 candida alb
24	40	41.7	1082	1 SP23_YEAST	P35210 saccharomyc
25	40	41.7	1136	1 NOS2_CHICK	O90703 gallus gall
26	39	40.6	158	1 YGJK_YEAST	P53218 saccharomyc
27	39	40.6	197	1 TMRB_BACSU	P12921 bacillus su
28	39	40.6	283	1 Y1JO_ECOLI	P12677 escherichia
29	39	40.6	380	1 CAGD_MOUSE	O64689 mus musculu
30	39	40.6	518	1 TBX5_MOUSE	P70326 mus musculu
31	39	40.6	877	1 DP01_LACLC	O32801 lactococcus
32	39	40.6	1926	1 LPH_RABIT	P09849 oryctolagus
33	38.5	40.1	875	1 UE3A_HUMAN	O05086 homo sapien

## RESULT 1

ID	NS2A_HUMAN	STANDARD;	PRT;	1153 AA.
AC	P35228; Q16692; O60757; Q16263;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)			
DE	(INDUCIBLE NOS) (INOS) (HEPATOCTE NOS) (HEP-NOS).			
GN	NOS2A OR NOS2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=93234523; PubMed=7682706;			
RA	Geller D.A., Lowenstein C.J., Shapiro R.A., Nussler A.K.,			
RA	di Silvio M., Wang S.C., Nakayama D.K., Simmons R.L., Snyder S.H.,			
RA	Billiar T.R.;			
RT	"Molecular cloning and expression of inducible nitric oxide synthase			
RT	from human hepatocytes.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 90:3491-3495(1993).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Colorectal adenocarcinoma;			
RC	MEDLINE=94032282; PubMed=7692964;			
RX	Sherman P.A., Laubach V.E., Reep B.R., Wood E.R.;			
RA	"Purification and cDNA sequence of an inducible nitric oxide synthase			
RT	from a human tumor cell line.";			
RT	Biochemistry 32:11600-11605(1993).			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Chondrocytes;			
RC	MEDLINE=94068614; PubMed=7504305;			
RX	Charles I.G., Palmer R.M.J., Hickery M.S., Bayliss M.T.,			
RA	Chubb A.P., Hall V.S., Moss D.W., Moncada S.;			
RT	"Cloning, characterization, and expression of a cDNA encoding an			
RT	inducible nitric oxide synthase from the human chondrocyte.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 90:11419-11423(1993).			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Articular chondrocytes;			
RC	MEDLINE=94368816; PubMed=7522054;			
RX	Maier R., Bilbe G., Rediske J., Lotz M.;			
RA	"Inducible nitric oxide synthase from human articular chondrocytes:			
RT	cDNA cloning and analysis of mRNA expression.";			
RT	Biochim. Biophys. Acta 1208:145-150(1994).			
RL	[5]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Retina;			
RC	MEDLINE=95091827; PubMed=7528017;			
RX	Park C.S., Pardhasaradhi K., Gianotti C., Villegas E., Krishna G.;			
RA	"Human retina expresses both constitutive and inducible isoforms of			
RT	nitric oxide synthase mRNA.";			

34	38	39.6	344	1	RPOA_SPIMX	O98462 spirogyra m
35	38	39.6	536	1	GLCM_HUMAN	P04062 homo sapien
36	38	39.6	571	1	PTI_BUCAI	Q9wx16 buchnera ap
37	38	39.6	688	1	LIP_STAEP	Q02510 staphylococ
38	38	39.6	739	1	PEC1_BOVIN	P51866 bos taurus
39	38	39.6	776	1	CME3_BACSU	P39695 bacillus su
40	38	39.6	821	1	YQIG_ECOLI	P76655 escherichia
41	38	39.6	885	1	UE3A_MOUSE	O08759 mus musculu
42	38	39.6	925	1	YE9G_SCHPO	O13776 schizosacch
43	38	39.6	1046	1	TFIA_HUMAN	O15164 homo sapien
44	38	39.6	1071	1	UBP7_YEAST	P40453 saccharomyc
45	38	39.6	1656	1	ATC8_YEAST	Q12674 saccharomyc

## ALIGNMENTS

RL Biochem. Biophys. Res. Commun. 205:85-91(1994).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Glioblastoma.  
 RX MEDLINE-95155267; PubMed-7531687;  
 RA Hokari A., Zeniya M., Esumi H.;  
 RT "Cloning and functional expression of human inducible nitric oxide  
 RT synthase (NOS) cDNA from a glioblastoma cell line A-172.";  
 RL J. Biochem. 116:575-581(1994).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Airway epithelium;  
 RX MEDLINE-95373268; PubMed-7544004;  
 RA Guo F.H., de Raevae R.H., Rice T.W., Stuehr D.J., Thunnissen F.B.J.M.,  
 RA Erzurum S.C.;  
 RT "Continuous nitric oxide synthesis by inducible nitric oxide synthase  
 RT in normal human airway epithelium in vivo.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7809-7813(1995).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Cardiac myocytes;  
 RX MEDLINE-97304504; PubMed-9160867;  
 RA Luss H., Li R.-K., Shapiro R.A., Tzeng E., McGowan F.X., Yoneyama T.,  
 RA Hatakeyama K., Geller D.A., Mickie D.A.G., Simmons R.L.,  
 RA Billiar T.R.;  
 RT "Differentiated human ventricular cardiac myocytes express  
 RT inducible nitric oxide synthase mRNA but not protein in response to  
 RT IL-1, TNF, IFN-gamma, and LPS.";  
 RL J. Mol. Cell. Cardiol. 29:1153-1165(1997).  
 RN [9]  
 RP SEQUENCE OF 380-473 FROM N.A.  
 RC TISSUE-Kidney;  
 RX MEDLINE-95165725; PubMed-7532248;  
 RA McJay J.S., Chatterjee P., Nicolson A.G., Jardine A.G., McKay N.G.,  
 RA Ralston S.H., Grabowski P., Haites N.E., Macleod A.M.,  
 RA Hawksworth G.M.;  
 RT "Nitric oxide production by human proximal tubular cells: a novel  
 RT immunomodulatory mechanism?";  
 RL Kidney Int. 46:1043-1049(1994).  
 RN [10]  
 RP CHARACTERIZATION.  
 RX MEDLINE-96047340; PubMed-7558036;  
 RA Bloch K.D., Wolfgram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G.,  
 RA Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;  
 RT "Three members of the nitric oxide synthase II gene family (NOS2A,  
 RT NOS2B, and NOS2C) colocalize to human chromosome 17.";  
 RL Genomics 27:526-530(1995).  
 RN [11]  
 RP CHARACTERIZATION.  
 RX MEDLINE-9839865; PubMed-9721329;  
 RA Taylor B.S., Alarcon L.H., Billiar T.R.;  
 RT "Inducible nitric oxide synthase in the liver: regulation and  
 RT function.";  
 RL Biochimica 63:766-781(1998).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 74-504.  
 RX MEDLINE-99340067; PubMed-10409685;  
 RA Li H., Raman C.S., Glaser C.B., Blasko E., Young T.A., Parkinson J.F.,  
 RA Whitlow M., Poulos T.L.;  
 RT "Crystal structures of zinc-free and -bound heme domain of human  
 RT inducible nitric-oxide synthase. Implications for dimer stability and  
 RT comparison with endothelial nitric-oxide synthase.";  
 RL J. Biol. Chem. 274:21276-21284(1999).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 82-528.  
 RX MEDLINE-99173237; PubMed-10074942;  
 RA Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,  
 RA Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Natula S.K.,  
 RA Weber P.C.;  
 RT "Structural characterization of nitric oxide synthase isoforms  
 RT reveals striking active-site conservation.";  
 RL Nat. Struct. Biol. 6:233-242(1999).  
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE

CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO  
 CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.  
 CC -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + H<sup>+</sup> O(2) -> CITRULLINE +  
 CC NITRIC OXIDE + N NADP(+).  
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 CC TETRAHYDROBIPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 CC THE ENZYME (BY SIMILARITY).  
 CC -1- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST  
 CC WITH MOUSE NOS2). ASPIRIN INHIBITS EXPRESSION AND FUNCTION OF THIS  
 CC ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF  
 CC TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE  
 CC CATALYTIC ACTIVITY (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE LIVER, RETINA, BONE CELLS AND  
 CC AIRWAY EPITHELIAL CELLS OF THE LUNG. NOT EXPRESSED IN THE  
 CC PLATELETS.  
 CC -1- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES.  
 CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
 CC -----  
 CC EMBL; L09210; AAA59171.1; -;  
 CC EMBL; L24553; AAA36375.1; -;  
 CC EMBL; X73029; CAA51512.1; -;  
 CC EMBL; U05810; AAA56666.1; -;  
 CC EMBL; U31511; ABA49041.1; -;  
 CC EMBL; D26525; BAA05531.1; -;  
 CC EMBL; U20141; AAB60366.1; -;  
 CC EMBL; AF068236; AAC19133.1; -;  
 CC EMBL; S75615; AAD14179.1; -;  
 CC PIR; A47475; A47475.  
 CC PDB; 1NSI; 07-JAN-00.  
 CC PDB; 2NSI; 07-JAN-00.  
 CC PDB; 4NOS; 04-FEB-00.  
 CC MIN; 163730; -;  
 CC InterPro; IPR001094; -;  
 CC InterPro; IPR001433; -;  
 CC InterPro; IPR001709; -;  
 CC InterPro; IPR003097; -;  
 CC Pfam; PF00667; FAD\_binding; 1.  
 CC Pfam; PF00175; oxidored\_fad; 1.  
 CC PRINTS; PR00369; FLAVODOXIN.  
 CC PRINTS; PR00371; FPNCR.  
 CC KW Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;  
 CC Heme; Phosphorylation; Zinc; Metal-binding; Multigene family;  
 CC 3D-structure.  
 CC BINDING 200 200 HEME.  
 CC DOMAIN 509 529 CALMODULIN-BINDING (POTENTIAL).  
 CC NP\_BIND 623 654 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 CC NP\_BIND 767 778 FAD (ADP PART) (BY SIMILARITY).  
 CC NP\_BIND 903 913 FAD (FLAVIN PART) (BY SIMILARITY).  
 CC NP\_BIND 978 996 NADP (RIBOSE PART) (BY SIMILARITY).  
 CC NP\_BIND 1076 1091 NADP (ADP PART) (BY SIMILARITY).  
 CC METAL 110 110 ZINC.  
 CC METAL 115 115 ZINC.  
 CC MOD\_RES 234 234 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 CC MOD\_RES 578 578 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 CC MOD\_RES 892 892 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 CC CONFLICT 23 23 D -> G (IN REF. 4).  
 CC CONFLICT 154 154 F -> L (IN REF. 4).  
 CC CONFLICT 177 177 R -> V (IN REF. 4).  
 CC CONFLICT 266 266 G -> H (IN REF. 8).  
 CC CONFLICT 423 423 L -> I (IN REF. 2).  
 CC CONFLICT 439 439 A -> T (IN REF. 8).  
 CC CONFLICT 439 439 S -> L (IN REF. 5 AND 6).  
 CC CONFLICT 608 608 T -> I (IN REF. 7).  
 CC CONFLICT 676 676 T -> A (IN REF. 4).  
 CC CONFLICT 800 800

Query Match 100.0%; Score 96; DB 1; Length 1153;  
Best Local Similarity 100.0%; Pred. No. 2.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVTQDDLOVHNLKSKOON 18  
Db 37 SPVTQDDLOVHNLKSKOON 54

RESULT 2  
ID NOS2\_MACMU STANDARD; PRT; 162 AA.  
AC 046660;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)  
DE (INDUCIBLE NOS) (INOS) (FRAGMENT).  
GN NOS2.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Microglia;  
RX MEDLINE=97056192; PubMed=8900532;  
RA Lane T.E., Buchmeier M.J., Watry D.D., Fox H.S.;  
RT "Expression of inflammatory cytokines and inducible nitric oxide  
synthase in brains of HIV-infected rhesus monkeys: applications to  
HIV-induced central nervous system disease.";  
RL Mol. Med. 2:27-37(1996).  
CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. INOS AND NO MAY  
CONTRIBUTE TO SIMIAN IMMUNODEFICIENCY VIRUS (SIV)-INDUCED CENTRAL  
NERVOUS SYSTEM DISEASE.  
CC -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +  
NITRIC OXIDE + N NADP(+).  
CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
THE ENZYME (BY SIMILARITY).  
CC -1- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY  
SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- INDUCTION: BY LIPOPOLYSACCHARIDES.  
CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; U31907; AAC39525.1; -  
CC HSSP; P29477; INOC.  
CC Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;  
KW Multigene family.  
FT NON\_TER 1  
FT NON\_TER 162 162  
SQ SEQUENCE 162 AA; 17813 MW; 0457464D32287065 CRC64;

Query Match 84.4%; Score 81; DB 1; Length 162;  
Best Local Similarity 88.9%; Pred. No. 9.4e-07;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPVTQDDLOVHNLKSKOON 18  
Db 17 SLVTQDDLOVHNLKSKOON 34

RESULT 3  
ID T3MH\_HAEIN STANDARD; PRT; 629 AA.  
AC 071366;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE PUTATIVE TYPE III RESTRICTION-MODIFICATION SYSTEM HINDVIP ENZYME MOD  
DE (EC 2.1.1.72) (HINDVIP METHYLTRANSFERASE) (M.HINDVIP).  
GN H11056  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RD / KW20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
RD.";  
RL Science 269:496-512(1995).  
CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA ADENINE =  
S-ADENOSYL-L-HOMOCYSTEINE + DNA 6-METHYLAMINOPURINE.  
CC -1- SUBUNIT: CONTAINS TWO DIFFERENT SUBUNITS: RES AND MOD. MOD IS  
A HOMOTETRAMER (BY SIMILARITY).  
CC -1- SIMILARITY: WITH OTHER TYPE III MOD PROTEINS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; U32786; AAC22721.1; -  
CC TIGR; H11056; -  
CC REBASE; 3701; M.Hindorf1056P.  
CC InterPro; IPR001091; -  
CC InterPro; IPR002052; -  
CC InterPro; IPR002295; -  
CC InterPro; IPR002941; -  
CC Pfam; PF01555; N6\_N4\_Mtase; 1.  
CC PRINTS; PR00506; D21N6MTFRASE.  
CC PRINTS; PR00508; S21N6MTFRASE.  
CC PROSITE; PS00092; N6\_MTASE; 1.  
CC KW Hypothetical protein; Transferase; Methyltransferase; DNA-binding;  
KW Restriction system.  
SQ SEQUENCE 629 AA; 71845 MW; 93ADAD909DB41E84 CRC64;

Query Match 46.9%; Score 45; DB 1; Length 629;  
Best Local Similarity 63.6%; Pred. No. 5.9;  
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 DDQYHNLKSKQ 16  
Db 415 DDQYHNLKSKQ 425

RESULT 4  
YNP9\_CAEEL

```

ID YNP9_CAEEL STANDARD; PRT; 705 AA.
AC P34562;
DT 01-FEB-1994 (Rel. 28, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HYPOTHETICAL 80.6 KDA PROTEIN T05G5.9 IN CHROMOSOME III.
GN T05G5.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sultson J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RN Nature 368:32-38(1994).
RL [2]
RN REVISIONS.
RC STRAIN=BRISTOL N2;
RA Durbin R.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z27079; CAA81596.1; -.
DR PIR; S41009; S41009.
DR WormPep; T05G5.9; CE21153.
DR InterPro; IPR000237; -.
DR Pfam; PF01465; Grip; 1.
KW Hypothetical protein; Coiled coil.
FT DOMAIN 75 137 COILED COIL (POTENTIAL).
FT DOMAIN 160 509 COILED COIL (POTENTIAL).
FT DOMAIN 562 641 COILED COIL (POTENTIAL).
SQ SEQUENCE 705 AA; 80637 MW; 9E89873F5FC04966 CRC64;

Query Match 46.9%; Score 45; DB 1; Length 705;
Best Local Similarity 37.5%; Pred. No. 6.7;
Matches 6; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 3 VTQDDQLQYHNLKQQN 18
DB 203 ITENDLVNMMKKN 218

RESULT 5
PANEL_PSEFL
ID PANEL_PSEFL STANDARD; PRT; 266 AA.
AC Q92EP8;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
DE (KETOPANTOATE HYDROXYMETHYLTRANSFERASE).

us-08-833-506c-26.rsp
```

```

GN PANB.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SBW25;
RA Rainey P.B.;
RT "Adaptation of Pseudomonas fluorescens to the plant rhizosphere.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 5,10-METHYLENETETRAHYDROFOLATE +
CC 3-METHYL-2-OXOBUTANOATE -> TETRAHYDROFOLATE + 2-DEHYDROANTOATE.
CC -1- PATHWAY: FIRST ENZYME OF THE PANTOTHENATE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE PANB FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ130846; CAA10222.1; -.
KW Transferase; Methyltransferase.
SQ SEQUENCE 266 AA; 27969 MW; 51B59D25C30E03F3 CRC64;

Query Match 45.8%; Score 44; DB 1; Length 266;
Best Local Similarity 61.5%; Pred. No. 3.1;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PVTQDDQLQYHNL 14
DB 59 PVTTDLAYHTAS 71

RESULT 6
YHCS_HAEIN
ID YHCS_HAEIN STANDARD; PRT; 288 AA.
AC P43011;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL TRANSCRIPTIONAL REGULATOR H11364 (ORF2).
GN H11364.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX PubMed=8635745;
RA Chandler M.S., Smith R.A.;
RT "Characterization of the Haemophilus influenzae topA locus: DNA
RT topoisomerase I is required for genetic competence.";
RL Gene 169:25-31(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
```

DR	PTR; B25123; OXCKX5.
DR	InterPro; IPR002655; -;
DR	pfam; PF01756; ACOX; 1.
KW	Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoprotein; PAD;
KW	Multigene family.
FT	INIT_MET 0
SQ	SEQUENCE 561 AA; 74132 MW; 99F89CADEE2D3B0A CRC64;
Query Match	43.8%; Score 42; DB 1; Length 661;
Best Local Similarity	43.8%; Pred.No. 20;
Matches	7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY	2 PVTQDDLYHNLKQQ 17
Dd	: :   :  :  :  :
Db	43 PILKVDSYNYLTKDQ 58
RESULT 8	
MURE_BUCAI	
ID	MURE_BUCAI STANDARD; PRT; 497 AA.
AC	P57316;
DT	01-OCT-2000 (Rel. 40, Created)
DT	01-OCT-2000 (Rel. 40, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	UDP-N-ACETYL-MURAMOYLALANYL-D-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE
DE	(EC 6.3.2.13) (UDP-N-ACETYLMURAMYL-TRIPEPTIDE SYNTHETASE) (MESO-
DE	DIAMINOPIMELATE-ADDING ENZYME) (UDP-MURNAC-TRIPEPTIDE SYNTHETASE).
GN	MURE OR BU221.
OS	Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS	symbiotic bacterium).
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX	NCB1_TaxID=118099;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=TOKYO 1998;
RX	MEDLINE=20445173; PubMed=1093077;
RA	Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT	"Genome sequence of the endocellular bacterial symbiont of aphids
RT	Buchnera sp. APS.";
RL	Nature 407:81-86(2000).
CC	-1- FUNCTION: CELL WALL FORMATION. DIAMINOPIMELIC ACID ADDING ENZYME
CC	(BY SIMILARITY).
CC	-1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANYL-D-
CC	GLUTAMATE + MESO-2,6-DIAMINOHEPTANEDIOATE = ADP + ORTHOPHOSPHATE
CC	+ UDP-N-ACETYLMURAMOYL-L-ALANYL-D-GLUTAMYL-MESO-2,6-
CC	DIAMINOHEPTANEDIOATE.
CC	-1- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC	-1- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation on
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AP001118; BAB12937.1; -.
KW	Peptidoglycan synthetasis; Cell wall; Cell division; Ligase;
KW	ATP-binding.
FT	NP_BIND 116 122 ATP (POTENTIAL).
SQ	SEQUENCE 497 AA; 56982 MW; 2BE0CC808B370FBF CRC64;
Query Match	43.2%; Score 41.5; DB 1; Length 497;
Best Local Similarity	52.9%; Pred.No. 17;
Matches	9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
QY	3 VTQDDLYH-NLSKQON 18
Dd	:  :  :  :  :  :  :
Db	207 LTQDHLDYHENLEKYES 223

```

RESULT 9
NOS2_RAT
ID NOS2_RAT STANDARD; PRT: 1147 AA.
AC Q06518; P97774; Q35765; Q35766; Q64558; Q64005; Q63267;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
DE (INDUCIBLE NOS) (INOS).
GN NOS2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN RP SEQUENCE FROM N.A.
RN RC TISSUE-Vascular smooth muscle;
RN RX MEDLINE=93191721; PubMed=7680561;
RA Nunokawa Y., Ishida N., Tanaka S.;
RT "Cloning of inducible nitric oxide synthase in rat vascular smooth
RT muscle cells.";
RL Biochem. Biophys. Res. Commun. 191:89-94(1993).
[2]
RN RP SEQUENCE FROM N.A.
RN RC STRAIN-Wistar; TISSUE-Pancreatic islets;
RN RX MEDLINE=93309542; PubMed=7540573;
RA Karlsten A.E., Andersen H.O., Vissing H., Larsen P.M., Fey S.J.,
RA Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,
RA Mandrup-Poulsen T., Boel E., Nerup J.;
RT "Cloning and expression of cytokine-inducible nitric oxide synthase
RT cDNA from rat islets of Langerhans.";
RL Diabetes 44:753-758(1995).
[3]
RN RP SEQUENCE FROM N.A.
RN RC STRAIN-SPRAGUE-Dawley; TISSUE-Astrocytes;
RN RX MEDLINE=94231594; PubMed=7513765;
RA Galea E., Reits D.J., Feinstein D.L.;
RT "Cloning and expression of inducible nitric oxide synthase from rat
RT astrocytes.";
RL J. Neurosci. Res. 37:406-414(1994).
[4]
RN RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RN RC TISSUE-Liver;
RN RX MEDLINE=94039059; PubMed=7693462;
RA Adachi H., Iida S., Oguchi S., Onshima H., Suzuki H., Nagasaki K.,
RA Kawasaki H., Sugimura T., Esumi H.;
RT "Molecular cloning of a cDNA encoding an inducible
RT calmodulin-dependent nitric-oxide synthase from rat liver and its
RT expression in COS 1 cells.";
RL Eur. J. Biochem. 217:37-43(1993).
[5]
RN RP SEQUENCE FROM N.A.
RN RC STRAIN-SPRAGUE-Dawley; TISSUE-Hepatocytes;
RN RX MEDLINE=93221515; PubMed=7682072;
RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
RT "Hepatocytes and macrophages express an identical cytokine inducible
RT nitric oxide synthase gene.";
RL Biochem. Biophys. Res. Commun. 191:767-774(1993).
[6]
RN RP SEQUENCE FROM N.A.
RN RC STRAIN-SPRAGUE-Dawley; TISSUE-Aorta;
RN RX MEDLINE=94325351; PubMed=7519448;
RA Geng Y.J., Almqvist M., Hansson G.K.;
RT "cDNA cloning and expression of inducible nitric oxide synthase from
RT rat vascular smooth muscle cells.";
RL Biochim. Biophys. Acta 1218:421-424(1994).
[7]
RN RP SEQUENCE FROM N.A.
RN RA Kosuga K., Yui Y., Hattori R., Sase K., Ezawa H., Aoyama T.,
RA Inoue R., Sasayama S.;
RT "Cloning of an inducible nitric oxide synthase from rat

```

```

RT polymorphonuclear neutrophils.";
RL Endothelium 2:217-221(1994).
[8]
RN RP SEQUENCE FROM N.A.
RN RX MEDLINE=97070590; PubMed=8913516;
RA Tsutsumishita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,
RA Futaki S., Niwa M.;
RT "Sequence analysis of inducible nitric oxide synthase in rat kidney,
RT lung, and uterus.";
RL Biol. Pharm. Bull. 19:1374-1376(1996).
[9]
RN RP SEQUENCE OF 426-788 FROM N.A.
RN RC STRAIN-DAHL/RAPP SALT SENSITIVE STRAIN; TISSUE-Vascular smooth muscle;
RN RX MEDLINE=98195092; PubMed=9535415;
RA Chen P.Y., Gladish R.D., Sanders P.W.;
RT "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp
RT salt-sensitive rats.";
RL Hypertension 31:918-924(1998).
[10]
RN RP SEQUENCE OF 509-740 FROM N.A.
RN RC STRAIN-Wistar; TISSUE-Renal glomerulus;
RA Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;
RT "Advances in the studies of NO synthesis regulation in mesangial
RT cells.";
RL Nephrologia 16:35-39(1996).
[11]
RN RP SEQUENCE OF 479-655 FROM N.A.
RN RC STRAIN-SPRAGUE-Dawley; TISSUE-Renal glomerulus;
RN RX MEDLINE=94276509; PubMed=7516453;
RA Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montani D.,
RA Klahr S.;
RT "Location of an inducible nitric oxide synthase mRNA in the normal
RT kidney.";
RL Kidney Int. 45:998-1005(1994).
[12]
RN RP SEQUENCE OF 420-479 FROM N.A.
RN RC TISSUE-Myocardium;
RA Michel T., Balligand J.-L.;
RT "Isolation and characterization of INOS from rat cardiocytes.";
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.
CC -|- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) -> CITRULLINE +
CC NITRIC OXIDE + N NADP(+).
CC -|- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME.
CC -|- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN
CC INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE
CC EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL
CC MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY
CC SIMILARITY).
CC -|- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -|- TISSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY IN THE
CC MEDULLARY THICK ASCENDING LIMB, WITH MINOR AMOUNTS IN THE
CC MEDULLARY COLLECTING DUCT AND VASA RECTA BUNDLE.
CC -|- INDUCTION: BY INTERFERON GAMMA AND LIPOPOLYSACCHARIDE.
CC -|- SIMILARITY: BELONGS TO THE NOS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D14051; BAA03138.1; -
DR EMBL; U26686; AAA85861.1; -
DR EMBL; U03699; AAC13747.1; -
DR EMBL; D12520; BAA02090.1; -
DR EMBL; L12562; AAA41720.1; -
DR EMBL; X76881; CAA54208.1; -

```

DR EMBL; D44591; BAA07994.1; -  
 DR EMBL; D83661; BAA12035.1; -  
 DR EMBL; AF008619; AAC18401.1; -  
 DR EMBL; AF008620; AAC18402.1; -  
 DR EMBL; U48829; AAB18620.1; -  
 DR EMBL; S71597; AAB31028.2; -  
 DR EMBL; L36063; AAC02242.1; -  
 DR PIR; JC1472; JC1472.  
 DR HSSP; P29477; INOC.  
 DR InterPro; IPR001094; -  
 DR InterPro; IPR001433; -  
 DR InterPro; IPR001709; -  
 DR InterPro; IPR003097; -  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR Pfam; PF00175; oxidoreduced\_fad; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;  
 KW Zinc; Metal-binding; Multigene family.  
 FT BINDING 197 197 HEME (BY SIMILARITY).  
 FT DOMAIN 506 526 FMN (PYRIMIDINE-BINDING (POTENTIAL)).  
 FT NP\_BIND 620 651 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FT NP\_BIND 764 775 FAD (ADP PART) (BY SIMILARITY).  
 FT NP\_BIND 900 910 FAD (FLAVIN PART) (BY SIMILARITY).  
 FT NP\_BIND 975 993 NADP (RIBOSE PART) (BY SIMILARITY).  
 FT NP\_BIND 1073 1088 NADP (ADP PART) (BY SIMILARITY).  
 FT METAL 107 107 ZINC (BY SIMILARITY).  
 FT METAL 112 112 ZINC (BY SIMILARITY).  
 FT CONFLICT 10 10 R -> K (IN REF. 7).  
 FT CONFLICT 72 72 H -> Y (IN REF. 1).  
 FT CONFLICT 107 107 C -> R (IN REF. 3).  
 FT CONFLICT 128 128 D -> V (IN REF. 8).  
 FT CONFLICT 130 130 P -> H (IN REF. 3).  
 FT CONFLICT 171 171 E -> G (IN REF. 8).  
 FT CONFLICT 195 195 P -> S (IN REF. 8).  
 FT CONFLICT 248 248 S -> T (IN REF. 3 AND 5).  
 FT CONFLICT 264 264 Y -> I (IN REF. 3).  
 FT CONFLICT 277 277 D -> E (IN REF. 3).  
 FT CONFLICT 348 348 A -> P (IN REF. 1).  
 FT CONFLICT 349 349 V -> A (IN REF. 6).  
 FT CONFLICT 380 380 F -> L (IN REF. 2, 7 AND 8).  
 FT CONFLICT 395 395 R -> S (IN REF. 4).  
 FT CONFLICT 412 412 V -> A (IN REF. 3).  
 FT CONFLICT 477 477 M -> I (IN REF. 12).  
 FT CONFLICT 513 513 T -> R (IN REF. 10).  
 FT CONFLICT 515 515 L -> W (IN REF. 11).  
 FT CONFLICT 545 545 G -> R (IN REF. 11).  
 FT CONFLICT 551 551 A -> R (IN REF. 10).  
 FT CONFLICT 556 556 A -> S (IN REF. 11).  
 FT CONFLICT 564 564 T -> N (IN REF. 11).  
 FT CONFLICT 570 570 E -> D (IN REF. 11).  
 FT CONFLICT 583 583 L -> P (IN REF. 5 AND 9).  
 FT CONFLICT 591 591 G -> A (IN REF. 11).  
 FT CONFLICT 591 591 G -> V (IN REF. 1 AND 6).  
 FT CONFLICT 619 619 A -> R (IN REF. 2).  
 FT CONFLICT 664 664 D -> G (IN REF. 10).  
 FT CONFLICT 679 680 Q -> VP (IN REF. 1).  
 FT CONFLICT 690 690 Q -> P (IN REF. 10).  
 Query Match 43.2%; Score 41.5; DB 1; Length 1147;  
 Best Local Similarity 55.6%; Pred. NO. 47;  
 Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;  
 QY 1 SPVTQDDQYHNLSKQON 18  
 || ||||| | | | |  
 Db 37 SPVTQDDPKSH---KHQ 51  
 RESULT 10  
 NS2D\_HUMAN  
 ID NS2D\_HUMAN STANDARD; PRT; 1147 AA.  
 AC O60591; O60604;  
 DT 30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)  
 01-OCT-2000 (Rel. 40, Last annotation update)  
 NITRIC OXIDE SYNTHASE, INDUCIBLE IID (EC 1.14.13.39) (NOS, TYPE II D)  
 (INDUCIBLE NOS) (INOS).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle, and Heart muscle;  
 RX MEDLINE=90066690; PubMed=9851365;  
 RA Adams V., Krabbes S., Jiang H., Yu J., Rahmel A., Gielen S.,  
 RA Schuler G., Hambrecht R.;  
 RT "Complete coding sequence of inducible nitric oxide synthase from  
 human heart and skeletal muscle of patients with chronic heart  
 failure.";  
 RT failure.";  
 RL Nitric Oxide 2:242-249(1998).  
 CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO  
 MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS. MAY BE INVOLVED IN  
 THE PATHOGENESIS OF DILATED CARDIOMYOPATHY OR OF EXERCISE  
 INTOLERANCE OBSERVED IN PATIENTS WITH CHRONIC HEART FAILURE.  
 CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) - CITRULLINE +  
 NITRIC OXIDE + N NADP(+).  
 CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 THE ENZYME (BY SIMILARITY).  
 CC -!- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (BY  
 SIMILARITY).  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE HEART AND SKELETAL MUSCLE  
 DURING CHRONIC HEART FAILURE, BUT NOT IN HEALTHY INDIVIDUALS.  
 CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
 -----  
 DR EMBL; AF049656; AAC83553.1; -  
 DR EMBL; AF051164; AAC83554.1; -  
 DR HSSP; P29477; INOC.  
 DR InterPro; IPR001094; -  
 DR InterPro; IPR001433; -  
 DR InterPro; IPR001709; -  
 DR InterPro; IPR003097; -  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR Pfam; PF00175; oxidoreduced\_fad; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 KW Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;  
 Heme; Zinc; Metal-binding; Multigene family.  
 FT BINDING 197 197 HEME (BY SIMILARITY).  
 FT DOMAIN 506 526 CALMODULIN-BINDING (POTENTIAL).  
 FT NP\_BIND 620 651 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FT NP\_BIND 764 775 FAD (ADP PART) (BY SIMILARITY).  
 FT NP\_BIND 900 910 FAD (FLAVIN PART) (BY SIMILARITY).  
 FT NP\_BIND 975 993 NADP (RIBOSE PART) (BY SIMILARITY).  
 FT NP\_BIND 1073 1088 NADP (ADP PART) (BY SIMILARITY).  
 FT METAL 107 107 ZINC (BY SIMILARITY).  
 FT METAL 112 112 ZINC (BY SIMILARITY).  
 FT CONFLICT 248 248 N -> S (IN AAC83554).  
 FT CONFLICT 271 271 D -> A (IN AAC83554).  
 FT CONFLICT 399 399 G -> E (IN AAC83554).  
 FT CONFLICT 640 640 P -> Q (IN AAC83554).  
 FT CONFLICT 731 731 A -> T (IN AAC83554).  
 FT CONFLICT 937 937 H -> N (IN AAC83554).  
 FT CONFLICT 1008 1009 TL -> NF (IN AAC83554).  
 FT CONFLICT 1024 1024 E -> K (IN AAC83554).

```
FT CONFLICT 1076 1076 I -> L (IN AAC83554).
FT CONFLICT 1129 1129 F -> V (IN AAC83554).
SQ SEQUENCE 1147 AA: 130528 MW: FF7E4C7ABA76D820 CRC64;

Query Match 43.2%; Score 41.5; DB 1; Length 1147;
Best Local Similarity 55.6%; Pred. No. 47;
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 1 SPVTQDDQLQYHNLKQON 18
DB 37 SPTQDDPKSH---KHQN 51

RESULT 11
NCAP_BUNSH STANDARD; PRT; 235 AA.
AC P03513;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE NUCLEOCAPSID PROTEIN (NUCLEOPROTEIN).
GN N.
OS Bunyavirus snowshoe hare.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Bunyavirus.
OX NCBI_TaxID=11580;
RN [1]
RP SEQUENCE FROM N.A.
RX BISHOP D.H.L., Gould K.G., Akashi H., Clerx-Van Haaster C.M.;
RT "The complete sequence and coding content of snowshoe hare bunyavirus
small (S) viral RNA species."
RL Nucleic Acids Res. 10:3703-3713(1982).
CC -!- SUBCELLULAR LOCATION: INTERNAL PROTEIN OF VIRUS PARTICLE..
CC -!- SIMILARITY: 45% IDENTITY TO AINO VIRUS NUCLEOPROTEIN N AND TO
SNOWSHOE HARE VIRUS NUCLEOPROTEIN N.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL: J02390; -; NOT_ANNOTATED_CDS.
DR PIR; A04103; VHVUNH.
DR InterPro; IPR001784; -.
DR Pfam; PF00952; Bunya_nucleocap: 1.
KW Nucleocapsid; RNA-binding.
SQ SEQUENCE 235 AA: 26770 MW: 687ED1D57AC097F8 CRC64;

Query Match 42.7%; Score 41; DB 1; Length 235;
Best Local Similarity 50.0%; Pred. No. 8;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SPVTQDDQLQYHNLK 14
DB 83 NPINSDDLTHRLS 96

RESULT 12
MURE_BUCAP STANDARD; PRT; 292 AA.
AC O85298;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UDP-N-ACETYLMURAMOYL-D-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE
(EC 6.3.2.13) (UDP-N-ACETYLMURAMOYL-TRIPETIDE SYNTHETASE) (MESO-
DIAMINOPIMELATE-ADDING ENZYME) (UDP-MURNAC-TRIPETIDE SYNTHETASE)
DE (FRAGMENT).

GN MURE.
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98353428; PubMed=9688822;
THAO M.L., Baumann P.;
RT "Sequence analysis of a DNA fragment from Buchnera aphidicola (Aphid
endosymbiont) containing the genes dapD-htrA-llvI-llvH-flsL-flsI-
mure."
RL Curr. Microbiol. 37:214-216(1998).
CC -!- FUNCTION: CELL WALL FORMATION. DIAMINOPIMELIC ACID ADDING ENZYME
(BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANYL-D-
GLUTAMATE + MESO-2,6-DIAMINOHEPTANEDIOATE -> ADP + ORTHOPHOSPHATE
+ UDP-N-ACETYLMURAMOYL-L-ALANYL-D-GLUTAMYL-MESO-2,6-
DIAMINOHEPTANEDIOATE.
CC -!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL: AF060492; AAC32338.1; -.
DR InterPro; IPR000713; -.
DR Pfam; PF01225; Mur_ligase: 1.
KW Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
ATP-binding.
KW NP_BIND 117 123 ATP (POTENTIAL).
FT NON_TER 292
SQ SEQUENCE 292 AA: 33467 MW: A4918644BF300AE8 CRC64;

Query Match 42.7%; Score 41; DB 1; Length 292;
Best Local Similarity 57.1%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 VTQDDQLQYHNLKQ 16
DB 207 LTQDHLQYHNMKQ 220

RESULT 13
RP3A_MOUSE STANDARD; PRT; 606 AA.
ID RP3A_MOUSE
AC P47708;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE RABPHILIN-3A (FRAGMENT).
GN RPH3A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=95122445; PubMed=7822236;
RA Inagaki N., Mizuta M., Saino S.;
RT "Cloning of a mouse Rbphilin-3A expressed in hormone-secreting
RT cells."
RL J. Biochem. 116:239-242(1994).
CC -!- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED WITH RAS-RELATED
PROTEIN RAB-3A IN SYNAPTIC VESICLE TRAFFIC AND/OR SYNAPTIC
VESICLE FUSION. COULD PLAY A ROLE IN NEUROTRANSMITTER RELEASE BY
```



```

Query Match      42.7%; Score 41; DB 1; Length 626;
Best Local Similarity 46.7%; Pred. No. 28;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 VTODDLQYHNLSKQQ 17
      || : || | : ||
Db      223 VLQERWRYHELQQQQ 237

RESULT 15
RP3A_RAT
ID RP3A_RAT STANDARD; PRT; 684 AA.

```

DT 01-FEB-1996 (Ref. 33, Last sequence update)  
 DT 15-JUL-1999 (Ref. 38, Last annotation update)  
 DE RABPHILIN-3A.  
 GN RPH3A.  
 OS Rattus norvegicus (Rat).

```

RX MEDLINE=95033210; PubMed=7946335;
RA Li C., Takei K., Geppert M., Daniell L., Stenius K., Chapman E.R.,
RA Jahn R., de Camilli P., Suedhof T.C.;
RT "Synaptic targeting of rabphilin-3A, a synaptic vesicle
RT Ca2+/phospholipid-binding protein, depends on rab3A/3C.";
RL Neuron 13:885-898(1994).
[2]
RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 44-167 IN COMPLEX WITH RAB3A.
RP TISSUE=Brain;
RC MEDLINE=991148269; PubMed=10025402;
RA Ostermeier C., Brunger A.T.;
RT "Structural basis of Rab effector specificity: crystal structure of
RT the small G protein Rab3A complexed with the effector domain of
RT rabphilin-3A.";
RL Cell 96:363-374(1999).
CC -I- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED WITH RAS-RELATED
CC PROTEIN RAB-3A IN SYNAPTIC VESICLE TRAFFIC AND/OR SYNAPTIC
CC VESICLE FUSION. COULD PLAY A ROLE IN NEUROTRANSMITTER RELEASE BY
CC REGULATING MEMBRANE FLOW IN THE NERVE TERMINAL.
CC -I- SUBUNIT: MONOMER.
CC -I- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN BRAIN.
CC -I- SIMILARITY: CONTAINS 2 C2 DOMAINS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; U12571; AAA62662.1;
DR PDB; 1ZBD; 12-APR-99.
DR InterPro; IPR000008;

```

DR InterPro; IPR001565; -  
DR InterPro; IPR001965; -  
DR Pfam; PF00168; C2; 2  
DR Pfam; PF00628; PHD; 1  
DR PRINTS; PR00360; C2DOMAIN.  
DR PRINTS; PR00399; SYNAPTOTAGMN.  
DR PROSITE; PS00499; C2\_DOMAIN\_1; 2.  
DR PROSITE; PS00004; C2\_DOMAIN\_2; 2.  
KW Repeat; Synapse; Protein transport; 3D-structure.  
FT DOMAIN 397 645 PHOSPHOLIPID BINDING (PROBABLE).  
FT DOMAIN 397 488 C2 DOMAIN.  
FT DOMAIN 557 645 C2 DOMAIN.  
SQ SEQUENCE 684 AA; 75832 MW; 05838BC3C7A86444 CRC64;

Query Match 42.7%; Score 41; DB 1; Length 684;  
Best Local Similarity 37.5%; Pred. No. 31;  
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 SPVTODDLQYHNLSKQ 16  
Db :||:||||:|:  
446 NPWNETLQYHGITEE 461

Search completed: September 10, 2001, 14:09:52  
Job time: 561 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: September 10, 2001, 14:01:13 ; Search time 42.28 Seconds  
(without alignments)  
32.430 Million cell updates/sec

Title: US-08-833-506c-26

Perfect score: 96  
Sequence: 1 SPVTQDDLOYHNLKQON 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	1153	2	A49676
2	45	46.9	629	2	C64180
3	45	46.9	690	2	S41009
4	43	44.8	288	2	D64171
5	43	44.8	447	2	T00906
6	43	44.8	647	2	JQ2149
7	43	44.8	1032	2	S61997
8	43	44.8	1801	2	T26774
9	43	44.8	1840	2	T30250
10	42	43.8	186	2	T51588
11	42	43.8	284	2	A82304
12	42	43.8	387	2	T15462
13	42	43.8	395	2	T25651
14	42	43.8	597	2	G83990
15	42	43.8	662	1	OXCKX5
16	41.5	43.2	497	2	A84956
17	41.5	43.2	1147	1	S47647
18	41.5	43.2	1147	1	I56575
19	41.5	43.2	1147	1	S38253
20	41.5	43.2	1147	1	I53165
21	41.5	43.2	1147	2	JC5027
22	41.5	43.2	1147	2	JC5028
23	41.5	43.2	1147	2	JC5029
24	41.5	43.2	1147	2	S65440
25	41	42.7	235	1	VHVUNH
26	41	42.7	488	2	E81403
27	41	42.7	626	2	S59435
28	41	42.7	681	2	JX0338
29	41	42.7	684	2	I58166

30	41	42.7	991	2	S57385	probable membrane
31	41	42.7	1192	2	A71623	probable secreted
32	41	42.7	1302	2	B41249	multidrug resistant
33	40	41.7	348	2	S11198	transforming prote
34	40	41.7	448	2	D85042	probable glycosyla
35	40	41.7	452	2	S37607	cyclin-like protei
36	40	41.7	542	1	E69600	two-component sens
37	40	41.7	761	1	TVHUMB	transforming prote
38	40	41.7	1009	2	S20538	chitin synthase (E
39	40	41.7	1082	2	S37837	suppressor protein
40	40	41.7	1535	2	T49042	hypothetical prote
41	39	40.6	140	2	G86413	hypothetical prote
42	39	40.6	158	2	S64321	hypothetical prote
43	39	40.6	197	1	YTBSY	tunicamycin resist
44	39	40.6	203	2	T34058	hypothetical prote
45	39	40.6	283	2	E65202	hypothetical trans

## ALIGNMENTS

RESULT 1

A49676  
nitric-oxide synthase (EC 1.14.13.39), inducible - human  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 20-Jun-2000  
C:Accession: A49676; JX0345; G01947; I38933; S47566; A47475  
R:Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; Hall, V.S.;  
Proc. Natl. Acad. Sci. U.S.A. 90, 11419-11423, 1993  
A:Title: Cloning, characterization, and expression of a cDNA encoding an inducible ni  
A:Reference number: A49676; MUID:94086614  
A:Accession: A49676  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1153 <RES>  
A:Cross-references: EMBL:X73029; NID:g441452; PIDN:CAA51512.1; PID:g441453  
R:Hokari, A.; Zeniya, M.; Esumi, H.  
J. Biochem. 116, 575-581, 1994  
A:Title: Cloning and functional expression of human inducible nitric oxide synthase (  
A:Reference number: JX0345; MUID:95155267  
A:Accession: JX0345  
A:Molecule type: mRNA  
A:Residues: 1-607, 'L', 609-1153 <HOK>  
A:Cross-references: DDBJ:D26525; NID:g559326; PIDN:BAA05531.1; PID:gl228940  
A:Experimental source: glioblastoma cell line A-172  
R:Park, C.; Park, R.; Krishna, G.  
Submitted to the EMBL Data Library, July 1995  
A:Reference number: G08912  
A:Accession: G01947  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-607, 'L', 609-1153 <PAR>  
A:Cross-references: EMBL:U31511; NID:g951320; PIDN:AAB49041.1; PID:g951321  
R:Guo, F.H.; De Raeye, H.R.; Rice, T.W.; Stuehr, D.J.; Thunnissen, F.B.; Erzurum, S.C  
Proc. Natl. Acad. Sci. U.S.A. 92, 7809-7813, 1995  
A:Title: Continuous nitric oxide synthesis by inducible nitric oxide synthase in norm  
A:Reference number: I38933; MUID:95372368  
A:Accession: I38933  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-675, 'I', 677-932, 'G', 934-965, 'A', 967-1153 <RE2>  
A:Cross-references: EMBL:U20141; NID:g687680; PIDN:AAB60366.1; PID:g687681  
R:Maier, R.; Bilbe, G.; Rediske, J.; Lotz, M.  
Biochim. Biophys. Acta 1208, 145-150, 1994  
A:Title: Inducible nitric oxide synthase from human articular chondrocytes: cDNA clon  
A:Reference number: S47566; MUID:94368816  
A:Accession: S47566  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-22, 'G', 24-153, 'L', 155-176, 'V', 178-799, 'A', 801-912, 'P', 914-1153 <MAI>  
A:Cross-references: EMBL:U05810; NID:g452487; PIDN:AAA56666.1; PID:g452488  
R:Geller, D.A.; Lowenstein, C.J.; Shapiro, R.A.; Nussler, A.K.; Di Silvio, M.; Wang,  
Proc. Natl. Acad. Sci. U.S.A. 90, 3491-3495, 1993

A:Title: Molecular cloning and expression of inducible nitric oxide synthase from human  
A:Reference number: A47475; MUID:93234523  
A:Accession: A47475  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-422, 'I', 424-804, 'D', 806-830, 'SP', 833-932, 'G', 934-965, 'A', 967-986, 'V', 988-1000  
A:Cross-references: GB:L09210; NID:9292241; PIDN:AAA59171.1; PID:9292242  
A:Experimental source: hepatocytes  
A>Note: sequence extracted from NCBI backbone (NCBIP:129733)  
C:Genetics:  
A:Gene: GDB:NOS2A; NOS2; INOS  
A:Cross-references: GDB:139215; OMIM:163730  
A:Map position: 17cen-17q11.2  
C:Function:  
A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH  
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reductase  
C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal  
F:509-529/Region: calmodulin binding #status predicted  
F:539-1127/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
F:541-677/Domain: flavodoxin homology <FLX>  
F:623-654/Region: FMN binding #status predicted  
F:765-778/Region: FAD-tyrosophosphate binding #status predicted  
F:903-913/Region: FAD-isoalloxazine binding #status predicted  
F:978-996/Region: NADP-ribose binding #status predicted  
F:1076-1091/Region: NADP-adenine binding #status predicted  
F:200/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 96; DB 2; Length 1153;  
Best Local Similarity 100.0%; Pred. No. 6e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVTQDDLYHNLSKQON 18  
|||||  
Db 37 SPVTQDDLYHNLSKQON 54

RESULT 2  
C64180  
hypothetical protein H1056 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 08-Oct-1999  
R:Accession: C64180  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: C64180  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-629 <TIGR>  
A:Cross-references: GB:U32786; GB:L42023; NID:g1574605; PIDN:AAC22721.1; PID:g1574609; C:Superfamily: conserved hypothetical protein H11364

Query Match 46.9%; Score 45; DB 2; Length 629;  
Best Local Similarity 63.6%; Pred. No. 14;  
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 DLIQYHNLSKQ 16  
||:|:|:|:  
Db 415 DLIQYNNLKE 425

RESULT 3  
S41009  
hypothetical protein T05G5.9 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Sep-1997  
R:Accession: S41009  
R:Thomas, K.

Query Match 44.8%; Score 43; DB 2; Length 447;  
Best Local Similarity 63.6%; Pred. No. 12;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PVTQDDLYHN 12  
| | | | | | | |  
Db 178 PVTQDDLYHN 188

RESULT 5  
T00906  
hypothetical protein F21B7.20 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C>Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 22-Oct-1999  
R:Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; eologis, A.; Ecker, J.R.  
A:Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.  
A:Reference number: Z14208  
A:Accession: T00906  
A:Status: translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-447 <SHI>  
A:Cross-references: EMBL:AC002560; NID:g2618677; PID:g2809251; GSPDB:GN00059; ATSP:F2  
C:Genetics:  
A:Gene: ATSP:F21B7.20  
A:Map position: 1  
A:Introns: 215/1; 240/2; 279/1

submitted to the EMBL Data Library, October 1993  
A:Reference number: S41001  
A:Accession: S41009  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-690 <THO>  
A:Cross-references: EMBL:227079; NID:g414641; PID:g414650  
C:Genetics:  
A:Introns: 13/3; 45/2; 68/3; 102/3; 135/3; 286/2; 323/3; 547/3; 565/1; 610/3

Query Match 46.9%; Score 45; DB 2; Length 690;  
Best Local Similarity 37.5%; Pred. No. 15;  
Matches 6; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 3 VTQDDLYHNLSKQON 18  
|:|:|:|:|:|:|:  
Db 203 ITENDLEVNMMKEKN 218

RESULT 4  
D64171  
hypothetical protein H11364 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 29-Sep-1999  
R:Accession: D64171  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: D64171  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-288 <TIGR>  
A:Cross-references: GB:U32816; GB:L42023; NID:g1574193; PIDN:AAC23011.1; PID:g1574196; C:Superfamily: conserved hypothetical protein H11364

Query Match 44.8%; Score 43; DB 2; Length 288;  
Best Local Similarity 63.6%; Pred. No. 12;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PVTQDDLYHN 12  
| | | | | | | |  
Db 178 PVTQDDLYHN 188

Best Local Similarity 61.1%; Pred. No. 20;  
Matches 11; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 3 VTODDLOY--HNLSKQON 18  
||||| | ||| |

Db 211 VTODDLYVFSNLSRVN 228

RESULT 6

QJ2149  
B west mating protein 2 (UhbW2) - smut fungus (Ustilago hordei)  
C:Species: Ustilago hordei (barley smut)  
C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 24-Sep-1999  
C:Accession: JQ2149, S33368  
R:Bakkeren, G.; Kronstad, J.W.  
Plant Cell 5, 123-136, 1993  
A:Title: Conservation of the b mating-type gene complex among bipolar and tetrapolar smu  
A:Reference number: S33365; MUID:93177212  
A:Accession: JQ2149  
A:Molecule type: DNA  
A:Residues: 1-647 <BAK>  
A:Cross-references: EMBL:218531; NID:g287659; PIDN:CAA79217.1; PID:g287661  
A:Experimental source: strain Uhl00, MAT-2, ade  
A:Comment: This protein controls mating and the establishment of the infectious dikaryon  
C:Genetics:  
A:Gene: BW  
A:Introns: 207/3  
C:Superfamily: unassigned homeobox proteins; homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F:161-217/Domain: homeobox homology <HGX>

Query Match 44.8%; Score 43; DB 2; Length 647;  
Best Local Similarity 47.1%; Pred. No. 31;  
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 SPVTODDLOYHNLSKQ 17  
||| |:: ||| |

Db 379 SPPTSDNVNLSNVSQO 395

RESULT 7

S61997  
hypothetical protein YPL125w - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein LPH2W  
C:Species: Saccharomyces cerevisiae  
C:Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 05-Nov-1999  
C:Accession: S61997  
R:Schlenstedt, G.; Silver, P.A.  
submitted to the EMBL Data Library, December 1995  
A:Reference number: S61996  
A:Accession: S61997  
A:Molecule type: DNA  
A:Residues: 1-1032 <SCH>  
A:Cross-references: EMBL:U43503; NID:g1163087; PID:g1163089; GSPDB:GN00016; MIPS:YPL125w  
C:Genetics:  
A:Gene: MIPS:YPL125w  
A:Map position: 16L

Query Match 44.8%; Score 43; DB 2; Length 1032;  
Best Local Similarity 41.2%; Pred. No. 54;  
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 PVTODDLOYHNLSKQON 18  
|::|::| |::|

Db 961 PLTAEQLRTHQLCKNND 977

RESULT 8

T26774  
hypothetical protein Y39G8C.b - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T26774  
R:Smye, R.  
submitted to the EMBL Data Library, October 1998  
A:Reference number: Z20263  
A:Accession: T26774  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1801 <WIL>  
A:Cross-references: EMBL:AL032634; PIDN:CAB54418.1; GSPDB:GN00019; CESP:Y39G8C.b  
A:Experimental source: clone Y39G8C  
C:Genetics:  
A:Gene: CESP:Y39G8C.b  
A:Map position: 1  
A:Introns: 69/3; 117/2; 186/3; 226/3; 371/3; 540/3; 857/1; 881/3; 1025/3; 1077

Query Match 44.8%; Score 43; DB 2; Length 1801;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 DDQLQYHNLSKQ 17  
| | | | | | | |

Db 598 DKLYRNISKQ 609

RESULT 9

T30250  
GT1 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
C:Accession: T30250  
R:Imai, Y.; Suzuki, Y.; Matsui, T.; Tohyama, M.; Wanaka, A.; Takagi, T.  
Brain Res. Mol. Brain Res. 31, 1-9, 1995  
A:Title: Cloning of a retinoic acid-induced gene, GT1, in the embryonal carcinoma cell  
A:Reference number: Z20788; MUID:96078271  
A:Accession: T30250  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-1840 <IMA>  
A:Cross-references: EMBL:D29801; NID:g475015; PIDN:BAA06184.1; PID:g475016  
A:Experimental source: brain  
A:Note: expression was specifically localized in neurons but not in glial cells

Query Match 44.8%; Score 43; DB 2; Length 1840;  
Best Local Similarity 53.3%; Pred. No. 1.1e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 TQDDLOYHNLSKQON 18  
||:| | ||:|

Db 282 TQETHYQNLAQYQH 296

RESULT 10

T51588  
hypothetical protein 2 [imported] - rice  
C:Species: Oryza sativa (rice)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 02-Sep-2000  
C:Accession: T51588  
R:Sawa, S.; Watanabe, K.; Okada, K.  
submitted to the EMBL Data Library, October 1998  
A:Reference number: Z25399  
A:Accession: T51588  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-186 <SAW>  
A:Cross-references: EMBL:AF098753; PIDN:AAC72848.1  
C:Superfamily: Arabidopsis thaliana hypothetical protein F6N15.22

Query Match 43.8%; Score 42; DB 2; Length 186;  
Best Local Similarity 50.0%; Pred. No. 11;

Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 QDDLOYHNLKSQON 18  
 ||:|: ||:|: ||:|  
 Db 66 QDNLKMHNSFRN 79

RESULT 11  
 A82304  
 3-methyl-2-oxobutanate hydroxymethyltransferase VC0592 [Imported] - Vibrio cholerae (strain 569B)  
 C:Species: Vibrio cholerae  
 C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
 C:Accession: A82304  
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, J.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000  
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A:Reference number: A82035; MUID:20406833  
 A:Accession: A82304  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-284 <HEI>  
 A:Cross-references: GB:AE004144; GB:AE003852; NID:g9655017; PIDN:AAF93759.1; GSPDB:GN001  
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C:Genetics:  
 A:Gene: VC0592  
 A:Map position: 1  
 C:Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase

Query Match 43.8%; Score 42; DB 2; Length 264;  
 Best Local Similarity 70.0%; Pred. No. 16;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PVTQDDLOYH 11  
 ||| ||: ||  
 Db 59 PVTVDIAH 68

RESULT 12  
 T15462  
 hypothetical protein C09B8.3 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 24-Nov-1999  
 C:Accession: T15462  
 R:Stellies, L.  
 submitted to the EMBL Data Library, June 1995  
 A:Description: The sequence of C. elegans cosmid C09B8.  
 A:Reference number: S61138  
 A:Accession: T15462  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-387 <STE>  
 A:Cross-references: EMBL:U29612; NID:g868273; PIDN:AAA68801.1; CESP:C09B8.3  
 A:Experimental source: strain Bristol N2  
 C:Genetics:  
 A:Gene: CESP:C09B8.3  
 A:Introns: 11/3; 61/1; 108/3; 144/3; 225/2; 275/2; 324/2; 352/3  
 C:Superfamily: Caenorhabditis elegans hypothetical protein C09B8.3

Query Match 43.8%; Score 42; DB 2; Length 387;  
 Best Local Similarity 53.3%; Pred. No. 25;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 TQDDLOYHNLKSQON 18  
 | : | | | | : | : |  
 Db 155 TLDNLQYKKNLFNERN 169

RESULT 13  
 T25651

hypothetical protein C47C12.6 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C:Accession: T25651  
 R:Connell, M.  
 submitted to the EMBL Data Library, August 1996  
 A:Description: The sequence of C. elegans cosmid C47C12.  
 A:Reference number: Z20062  
 A:Accession: T25651  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-395 <CON>  
 A:Cross-references: EMBL:U67951; PIDN:AAB07575.1; GSPDB:GN00028; CESP:C47C12.6  
 A:Experimental source: strain Bristol N2; clone C47C12  
 C:Genetics:  
 A:Gene: CESP:C47C12.6  
 A:Map position: X  
 A:Introns: 115/3; 148/3; 219/3; 252/3; 274/2; 322/1; 342/3

Query Match 43.8%; Score 42; DB 2; Length 395;  
 Best Local Similarity 50.0%; Pred. No. 26;  
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 SPVTQDDLOYHNLKSQ 16  
 ||:|: ||:|: ||:|  
 Db 298 SPSPNDNIFYNLSMQ 313

RESULT 14  
 GB3990  
 two-component sensor histidine kinase BH2727 [Imported] - Bacillus halodurans (strain 101-1)  
 C:Species: Bacillus halodurans  
 C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 31-Dec-2000  
 C:Accession: GB3990  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a  
 A:Reference number: A83650; MUID:20263314  
 A:Accession: GB3990  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-597 <STO>  
 A:Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BA806446.1; GSPDB:G  
 A:Experimental source: strain C-125  
 C:Genetics:  
 A:Gene: BH2727

Query Match 43.8%; Score 42; DB 2; Length 597;  
 Best Local Similarity 46.7%; Pred. No. 42;  
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 PVTQDDLOYHNLKSQ 16  
 ||| ||:|: ||:|  
 Db 144 PVTWDELQHAVTTE 158

RESULT 15  
 OXCKX5  
 acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxisomal - yeast (Candida tropicalis)  
 N:Alternate names: acyl-CoA oxidase I  
 C:Species: Candida tropicalis  
 C>Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 11-Jun-1999  
 C:Accession: B25123  
 R:Okazaki, K.; Takechi, T.; Kambara, N.; Fukui, S.; Kubota, I.; Kamiryo, T.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 1232-1236, 1986  
 A:Title: Two acyl-coenzyme A oxidases in peroxisomes of the yeast Candida tropicalis:  
 A:Reference number: A94084; MUID:86149279  
 A:Accession: B25123  
 A:Molecule type: DNA  
 A:Residues: 1-662 <OKA>  
 A:Cross-references: GB:M12161; NID:gl70913; PIDN:AAA34363.1; PID:gl70914

Search completed: September 10, 2001, 14:01:14  
Job time: 213 sec

**This Page Blank (uspto)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:01:55 ; Search time 35.97 Seconds  
(without alignments)  
10.304 Million cell updates/sec

Title: US-08-833-506c-26  
Perfect score: 96  
Sequence: 1 SPVTQDQLQYHNLKQKN 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	1146	4 US-09-126-109-12	Sequence 12, Appl
2	96	100.0	1153	1 US-08-314-917-2	Sequence 2, Appl
3	96	100.0	1153	1 US-08-265-046-2	Sequence 2, Appl
4	96	100.0	1153	2 US-08-465-522-2	Sequence 2, Appl
5	96	100.0	1153	5 PCT-US93-11401-2	Sequence 2, Appl
6	96	100.0	1153	5 PCT-US95-07849-2	Sequence 2, Appl
7	39	40.6	339	1 US-08-626-994A-3	Sequence 3, Appl
8	39	40.6	339	3 US-08-957-742-3	Sequence 3, Appl
9	39	40.6	351	2 US-08-929-417-2	Sequence 2, Appl
10	39	40.6	364	1 US-08-626-994A-1	Sequence 1, Appl
11	39	40.6	364	3 US-08-957-742-1	Sequence 1, Appl
12	39	40.6	833	1 US-08-073-384C-8	Sequence 8, Appl
13	39	40.6	833	1 US-08-254-359A-8	Sequence 8, Appl
14	39	40.6	833	1 US-08-483-043-8	Sequence 8, Appl
15	39	40.6	833	1 US-08-481-238-8	Sequence 8, Appl
16	39	40.6	833	2 US-08-471-066B-8	Sequence 8, Appl
17	39	40.6	833	2 US-08-484-956-8	Sequence 8, Appl
18	39	40.6	833	2 US-08-757-653-8	Sequence 8, Appl
19	39	40.6	833	2 US-08-599-491-8	Sequence 8, Appl
20	39	40.6	833	2 US-08-756-386-8	Sequence 8, Appl
21	39	40.6	833	2 US-08-623-516-8	Sequence 8, Appl
22	39	40.6	833	3 US-08-682-853A-8	Sequence 8, Appl
23	39	40.6	833	3 US-08-759-038-8	Sequence 8, Appl
24	39	40.6	833	3 US-08-758-314-8	Sequence 8, Appl
25	39	40.6	920	3 US-08-930-996A-8	Sequence 8, Appl
26	38.5	40.1	866	1 US-08-100-692-1	Sequence 1, Appl
27	38.5	40.1	866	2 US-08-674-030-1	Sequence 1, Appl

28	38.5	40.1	874	2	US-08-247-904B-8	Sequence 8, Appl
29	38.5	40.1	874	3	US-08-767-942A-21	Sequence 21, Appl
30	38	39.6	435	2	US-08-338-530A-2	Sequence 2, Appl
31	38	39.6	435	4	US-09-267-384-2	Sequence 2, Appl
32	38	39.6	494	4	US-09-198-956-2	Sequence 2, Appl
33	38	39.6	498	1	US-08-080-855-1	Sequence 1, Appl
34	38	39.6	546	2	US-08-713-928B-4	Sequence 4, Appl
35	37.5	39.1	1286	6	5206163-1	Patent No. 5206163
36	37	38.5	84	2	US-08-465-380-50	Sequence 50, Appl
37	37	38.5	84	2	US-08-465-380-51	Sequence 51, Appl
38	37	38.5	84	2	US-08-486-397-50	Sequence 50, Appl
39	37	38.5	84	2	US-08-486-397-51	Sequence 51, Appl
40	37	38.5	84	2	US-08-486-399-50	Sequence 50, Appl
41	37	38.5	84	2	US-08-486-399-51	Sequence 51, Appl
42	37	38.5	84	2	US-08-461-965-50	Sequence 50, Appl
43	37	38.5	84	2	US-08-461-965-51	Sequence 51, Appl
44	37	38.5	84	2	US-08-634-641-50	Sequence 50, Appl
45	37	38.5	84	3	US-09-249-448-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1  
US-09-126-109-12  
; Sequence 12, Application US/09126109  
; Patent No: 6171856  
; GENERAL INFORMATION:  
; APPLICANT: Thigpen, Anice  
; APPLICANT: Hohmeier, Hans-Ewald  
; APPLICANT: Newgard, Christopher B.  
; APPLICANT: Unger, Roger H.  
; APPLICANT: Shimabukuro, Michio  
; APPLICANT: Chen, Guaxun  
; APPLICANT: Rhodes, Christopher J.  
; APPLICANT: Hugl, Sigrun R.  
; APPLICANT: Cousin, Sharon  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
; TO NO-MEDIATED CYTOTOXICITY  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/126,109  
; FILING DATE: 30-JUL-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/055,092  
; FILING DATE: 30-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US Unknown  
; FILING DATE: 03-MAR-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMillian, Nabeela R.  
; REGISTRATION NUMBER: P-43,363  
; REFERENCE/DOCKET NUMBER: UTSD:560  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1146 amino acids  
; TYPE: amino acid

```
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-126-109-12

Query Match      100.0%; Score 96; DB 4; Length 1146;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVTODDLQYHNLSKQON 18
Db 37 SPVTODDLQYHNLSKQON 54

RESULT 2
US-08-314-917-2
; Sequence 2, Application US/08314917
; Patent No. 5468630
; GENERAL INFORMATION:
; APPLICANT: Billiar, Timothy R.
; APPLICANT: Nussler, Andreas K.
; APPLICANT: Geller, David A.
; APPLICANT: Simmons, Richard L.
; TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric
; TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold B. Silverman
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 600 Grant Street, 42nd Floor
; CITY: Pittsburgh
; STATE: PA
; COUNTRY: USA
; ZIP: 15219
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,917
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; APPLICATION NUMBER: US/07/981,344
; FILING DATE: 25-NOV-1992
; NAME: Silverman, Arnold B.
; REGISTRATION NUMBER: 22,614
; REFERENCE/DOCKET NUMBER: 116972
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (412) 566-6000
; TELEFAX: (412) 566-6099
; TELEX: 866172
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-314-917-2

Query Match      100.0%; Score 96; DB 1; Length 1153;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVTODDLQYHNLSKQON 18
Db 37 SPVTODDLQYHNLSKQON 54
```

```
RESULT 3
US-08-265-046-2
; Sequence 2, Application US/08265046
; Patent No. 5658565
; GENERAL INFORMATION:
; APPLICANT: Timothy R. Billiar
; APPLICANT: Edith Tzeng
; APPLICANT: Andreas K. Nussler
; APPLICANT: David A. Geller
; APPLICANT: Richard L. Simmons
; TITLE OF INVENTION: Inducible Nitric Oxide Synthase
; TITLE OF INVENTION: Gene for Treatment of Disease
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 1700 Market Street, Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,046
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Lewis F. Jr.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 119130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6020
; TELEFAX: (215) 575-6015
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-265-046-2

Query Match      100.0%; Score 96; DB 1; Length 1153;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVTODDLQYHNLSKQON 18
Db 37 SPVTODDLQYHNLSKQON 54

RESULT 4
US-08-465-522-2
; Sequence 2, Application US/08465522
; Patent No. 5882908
; GENERAL INFORMATION:
; APPLICANT: Billiar, Timothy R.
; APPLICANT: Nussler, Andreas K.
; APPLICANT: Geller, David A.
; APPLICANT: Simmons, Richard L.
; TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric
; TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 1700 Market St. Suite 3232
; CITY: Philadelphia
```

STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICANT: PatentIn Release #1.0, Version #1.25  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gould, Jr., Lewis F.  
REGISTRATION NUMBER: 25,057  
REFERENCE/DOCKET NUMBER: 116972-6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 575-6020  
TELEFAX: (215) 575-6015  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1153 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-465-522-2

Query Match 100.0%; Score 96; DB 2; Length 1153;  
Best Local Similarity 100.0%; Pred. No. 4.2e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVTQDDLOYNLSKQON 18  
DB 37 SPVTQDDLOYNLSKQON 54

RESULT 5  
PCT-US93-11401-2  
Sequence 2, Application PCTUS9311401  
GENERAL INFORMATION:  
APPLICANT: Billiar, Timothy R.  
APPLICANT: Nussler, Andreas K.  
APPLICANT: Geller, David A.  
APPLICANT: Simmons, Richard L.  
TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold B. Silverman  
ADDRESSEE: Eckert Seamans Cherin & Mellott  
STREET: 600 Grant Street, 42nd Floor  
CITY: Pittsburgh  
STATE: PA  
COUNTRY: USA  
ZIP: 15219  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICANT: PatentIn Release #1.0, Version #1.25  
FILING DATE: 25-NOV-1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/981,344  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Silverman, Arnold B.  
REGISTRATION NUMBER: 22,614  
REFERENCE/DOCKET NUMBER: 116972

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (412) 566-6000  
TELEFAX: (412) 566-6099  
TELEX: 866172  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1153 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-11401-2

Query Match 100.0%; Score 96; DB 5; Length 1153;  
Best Local Similarity 100.0%; Pred. No. 4.2e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVTQDDLOYNLSKQON 18  
DB 37 SPVTQDDLOYNLSKQON 54

## RESULT 6

PCT-US95-07849-2  
Sequence 2, Application PC/TUS9507849  
GENERAL INFORMATION:  
APPLICANT: University of Pittsburgh of the Commonwealth System of Higher  
APPLICANT: Education  
TITLE OF INVENTION: Inducible Nitric Oxide Synthase  
TITLE OF INVENTION: Gene for Treatment of Disease  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lewis F. Gould, Jr.  
ADDRESSEE: Eckert Seamans Cherin & Mellott  
STREET: 1700 Market Street, Suite 3232  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/07849  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gould, Lewis F. Jr.  
REGISTRATION NUMBER: 25,057  
REFERENCE/DOCKET NUMBER: 119130-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 575-6020  
TELEFAX: (215) 575-6015  
TELEX:

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1153 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-07849-2

Query Match 100.0%; Score 96; DB 5; Length 1153;  
Best Local Similarity 100.0%; Pred. No. 4.2e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVTQDDLOYNLSKQON 18  
DB 37 SPVTQDDLOYNLSKQON 54

```

;
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1+ (ASCII)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,742
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/626,994
; FILING DATE: April 3, 1996
; APPLICATION NUMBER: JP 77469/1995
; FILING DATE: April 3, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold Turk
; REGISTRATION NUMBER: 33,094
; REFERENCE/DOCKET NUMBER: P14595
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 716-1191
; TELEFAX: (703) 716-1180
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
;
US-08-957-742-3

Query Match 40.6%; Score 39; DB 3; Length 339;
Best Local Similarity 46.7%; Pred. No. 48;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 PVTDDLOYHNLSKQ 16
Db 287 PNTREDLPYHYDKK 301

RESULT 9
US-08-929-417-2
; Sequence 2, Application US/08929417
; Patent No. 5928895
; GENERAL INFORMATION:
; APPLICANT: Burnham, Martin K.
; TITLE OF INVENTION: No. 5928895el Iga Fc Binding Protein
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,417
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/027,030
; FILING DATE: 24-SEP-1996
; APPLICATION NUMBER: 60/040,656
; FILING DATE: 10-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dickinson, Q. Todd
; REGISTRATION NUMBER: 28,354
; REFERENCE/DOCKET NUMBER: P50545
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215/994-2252
; TELEFAX: 215/994-2222
; TELEX:

;
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1+ (ASCII)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,742
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/626,994
; FILING DATE: April 3, 1996
; APPLICATION NUMBER: JP 77469/1995
; FILING DATE: April 3, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold Turk
; REGISTRATION NUMBER: 33,094
; REFERENCE/DOCKET NUMBER: P14595
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 716-1191
; TELEFAX: (703) 716-1180
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
;
US-08-957-742-3

Query Match 40.6%; Score 39; DB 1; Length 339;
Best Local Similarity 46.7%; Pred. No. 48;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 PVTDDLOYHNLSKQ 16
Db 287 PNTREDLPYHYDKK 301

RESULT 8
US-08-957-742-3
; Sequence 3, Application US/08957742
; Patent No. 6017743
; GENERAL INFORMATION:
; APPLICANT: Shuichi TSUJI et al.
; TITLE OF INVENTION: Sia' 2,3Gala 1,4G1CNAc ` 2,8-
; TITLE OF INVENTION: STALYLTRANSFERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenblum & Bernstein, P.L.C.
; STREET: 1941 Roland Clarke Place
; CITY: Reston
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 20191
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1+ (ASCII)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/626,994A
; FILING DATE: April 3, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 77469/1995
; FILING DATE: April 3, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold Turk
; REGISTRATION NUMBER: 33,094
; REFERENCE/DOCKET NUMBER: P14595
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 716-1191
; TELEFAX: (703) 716-1180
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
;
US-08-626-994A-3

Query Match 40.6%; Score 39; DB 1; Length 339;
Best Local Similarity 46.7%; Pred. No. 48;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 PVTDDLOYHNLSKQ 16
Db 287 PNTREDLPYHYDKK 301

RESULT 8
US-08-957-742-3
; Sequence 3, Application US/08957742
; Patent No. 6017743
; GENERAL INFORMATION:
; APPLICANT: Shuichi TSUJI et al.
; TITLE OF INVENTION: Sia' 2,3Gala 1,4G1CNAc ` 2,8-
; TITLE OF INVENTION: STALYLTRANSFERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenblum & Bernstein, P.L.C.
; STREET: 1941 Roland Clarke Place
; CITY: Reston
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 20191
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 diskette
; COMPUTER: IBM PC compatible
;

```

```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 351 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; US-08-929-417-2
;
; Query Match          40.6%; Score 39; DB 2; Length 351;
; Best Local Similarity 46.2%; Pred. No. 50;
; Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
;
QY      6 DDLOYHNLKQON 18
DB      111 DDQKHHLQKEK 123
;
; RESULT 10
; US-08-626-994A-1
; Sequence 1, Application US/08626994A
; Patent No. 5798244
; GENERAL INFORMATION:
; APPLICANT: Shuichi TSUJI et al.
; TITLE OF INVENTION: Sia' 2,3Gala 1,4GlcNAc ' 2,8-
; TITLE OF INVENTION: SIALYLTRANSFERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenblum & Bernstein, P.L.C.
; STREET: 1941 Roland Clarke Place
; CITY: Reston
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 20191
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1+ (ASCII)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,742
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/626,994
; FILING DATE: April 3, 1996
; APPLICATION NUMBER: JP 77469/1995
; FILING DATE: April 3, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold Turk
; REGISTRATION NUMBER: 33,094
; REFERENCE/DOCKET NUMBER: PI4595
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 716-1191
; TELEFAX: (703) 716-1180
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 364 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: linear
; US-08-957-742-1
;
; Query Match          40.6%; Score 39; DB 3; Length 364;
; Best Local Similarity 46.7%; Pred. No. 52;
; Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
;
QY      2 PVTQDDLOYHNLKQ 16
DB      312 PNTREDLPYHYDKK 326
;
; RESULT 12
; US-08-073-384C-8
; Sequence 8, Application US/08073384C
; Patent No. 5541311
; GENERAL INFORMATION:
; APPLICANT: Dahlberg, James E.
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
; TITLE OF INVENTION: POLYMERASE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;
; Query Match          40.6%; Score 39; DB 1; Length 364;
; Best Local Similarity 46.7%; Pred. No. 52;
; Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
;
QY      2 PVTQDDLOYHNLKQ 16
DB      312 PNTREDLPYHYDKK 326
;
; RESULT 11
; US-08-957-742-1
```

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/073.384C  
; FILING DATE: 04-JUN-1993  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/986.330  
; FILING DATE: 07-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cartoll, Peter G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: FORS-00613  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/705-8410  
; TELEFAX: 415/397-8338  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 833 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-073-384C-8

Query Match 40.6%; Score 39; DB 1; Length 833;  
Best Local Similarity 41.2%; Pred. No. 1.4e+02;  
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 PVTQDDLOQYHNLSKQON 18  
I : : ||| I : : I  
Db 527 PIVEKILQYRELTKLKN 543

RESULT 13  
US-08-254-359A-8  
; Sequence 8, Application US/08254359A  
; Patent No. 5614402  
; GENERAL INFORMATION:  
; APPLICANT: DAHLBERG, JAMES E.  
; APPLICANT: LYAMICHEV, VICTOR I.  
; APPLICANT: BROW, MARY ANN D.  
; TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE  
; TITLE OF INVENTION: DNA POLYMERASE  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/254.359A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/073.384  
; FILING DATE: 06-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/986.330  
; FILING DATE: 07-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: FORS-01000

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 833 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-254-359A-8

Query Match 40.6%; Score 39; DB 1; Length 833;  
Best Local Similarity 41.2%; Pred. No. 1.4e+02;  
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 PVTQDDLOQYHNLSKQON 18  
I : : ||| I : : I  
Db 527 PIVEKILQYRELTKLKN 543

RESULT 14  
US-08-483-043-8  
; Sequence 8, Application US/08483043  
; Patent No. 5691142  
; GENERAL INFORMATION:  
; APPLICANT: Dahlberg, James E.  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA  
; TITLE OF INVENTION: POLYMERASE  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483.043  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/073.384  
; FILING DATE: 04-JUN-1993  
; APPLICATION NUMBER: US 07/986.330  
; FILING DATE: 07-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cartoll, Peter G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: FORS-00613  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/705-8410  
; TELEFAX: 415/397-8338  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 833 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-483-043-8

Query Match 40.6%; Score 39; DB 1; Length 833;  
Best Local Similarity 41.2%; Pred. No. 1.4e+02;

Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 PVTQDDLOYHNLKQON 18  
| : : ||| | : | : |  
Db 527 PIVEKILOYRELTCLKN 543

## RESULT 15

US-08-481-238-8  
; Sequence 8, Application US/08481238  
; Patent No. 5795763  
; GENERAL INFORMATION:  
; APPLICANT: DAHLBERG, JAMES E.  
; APPLICANT: LYAMICHEV, VICTOR I.  
; APPLICANT: BROW, MARY ANN D.  
; TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/481,238  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: FORS-01798  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 833 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-481-238-8

Query Match 40.6%; Score 39; DB 1; Length 833;  
Best Local Similarity 41.2%; Pred. NO. 1.4e+02;  
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 PVTQDDLOYHNLKQON 18  
| : : ||| | : | : |  
Db 527 PIVEKILOYRELTCLKN 543

Search completed: September 10, 2001, 14:01:56  
Job time: 225 sec

**This Page Blank (upto)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:00:24 ; Search time 67.08 Seconds  
(without alignments)  
16.268 Million cell updates/sec

Title: US-08-833-506c-26

Perfect score: 96

Sequence: 1 SPVQDDQLQYHNLKQQN 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

1:	/SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2:	/SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3:	/SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4:	/SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5:	/SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6:	/SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7:	/SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8:	/SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9:	/SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10:	/SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11:	/SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12:	/SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13:	/SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14:	/SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15:	/SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16:	/SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17:	/SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18:	/SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19:	/SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20:	/SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21:	/SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22:	/SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	18	AAW81222	Human iNOS peptide
2	96	100.0	18	AAW81178	Human iNOS (37-54)
3	96	100.0	18	AAW81278	Human iNOS peptide
4	96	100.0	18	AAW81204	Human iNOS peptide
5	96	100.0	18	AAW81208	Human iNOS peptide
6	96	100.0	1146	AAW96322	Inducible nitric o
7	96	100.0	1153	AAW55764	Sequence encoded b
8	96	100.0	1153	AAW63206	Nitric-oxide-synth
9	96	100.0	1153	AAW88464	Hepatocyte inducib
10	96	100.0	1153	AAW36113	Human inducible ni
11	96	100.0	1153	AAW31724	Amino acid sequenc

12	96	100.0	1153	22	AAW66724	Human inducible ni
13	81	84.4	15	19	AAW81223	Human iNOS peptide
14	81	84.4	15	19	AAW81288	Human iNOS peptide
15	80.5	83.9	17	19	AAW81263	Human iNOS peptide
16	80	83.3	15	19	AAW81227	Human iNOS peptide
17	80	83.3	15	19	AAW81292	Human iNOS peptide
18	80	83.3	15	19	AAW81267	Human iNOS peptide
19	67	69.8	12	19	AAW81228	Human iNOS peptide
20	67	69.8	12	19	AAW81293	Human iNOS peptide
21	67	69.8	12	19	AAW81268	Human iNOS peptide
22	65	67.7	12	19	AAW81224	Human iNOS peptide
23	65	67.7	12	19	AAW81289	Human iNOS peptide
24	50	52.1	9	19	AAW81225	Human iNOS peptide
25	50	52.1	9	19	AAW81290	Human iNOS peptide
26	46	47.9	9	19	AAW81229	Human iNOS peptide
27	46	47.9	9	19	AAW81294	Human iNOS peptide
28	46	47.9	9	19	AAW81264	Human iNOS peptide
29	45	46.9	550	21	AAW52422	Arabidopsis thalia
30	45	46.9	570	21	AAW52421	Arabidopsis thalia
31	45	46.9	616	21	AAW52420	Arabidopsis thalia
32	44	45.8	70	21	AAW02480	Human secreted pro
33	42	43.8	25	20	AAW41435	Fragment of human
34	42	43.8	25	20	AAW41436	Fragment of human
35	42	43.8	80	21	AAW38587	Human secreted pro
36	41.5	43.2	1147	17	AAW02571	Rat inducible nitr
37	41	42.7	9	19	AAW81265	Human iNOS peptide
38	41	42.7	10	19	AAW81270	Human iNOS peptide
39	41	42.7	258	22	AAW50082	Rat TNFR (p80) ext
40	41	42.7	487	22	AAW50084	TNFR:Fc fusion pro
41	41	42.7	1192	21	AAW18165	Plasmodium falcipa
42	40	41.7	57	21	AAW00549	Human secreted pro
43	40	41.7	64	21	AAW02530	Human secreted pro
44	40	41.7	85	21	AAW39159	Human secreted pro
45	40	41.7	415	21	AAW41567	Human ORFX ORF1331

#### ALIGNMENTS

RESULT 1

ID	AAW81222	standard; peptide; 18 AA.
XX		
AC	AAW81222;	
XX		
DT	30-APR-1999	(first entry)
XX		
DE	Human iNOS peptide fragment PS-5104.	
XX		
KW	Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;	
KW	monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;	
KW	myocardial infarction; tissue rejection; transplantation; psoriasis;	
KW	autoimmune disease; multiple sclerosis.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	18
FT		/note= "Asn residue amidated"
XX		
PN	WO9845710-A1.	
XX		
PD	15-OCT-1998.	
XX		
PF	11-APR-1997;	97WO-US06500.
XX		
PR	07-APR-1997;	97US-6667777.
XX		
PA	(WEBB/) WEBBER R.	
XX		
PI	Webber R;	
XX		
DR	WPI; 1998-594495/50.	



XX	30-APR-1999	(first entry)	
XX	Human iNOS peptide fragment capable of binding Mab 21C10-1D10 #2.		
XX	Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;		
XX	monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;		
XX	myocardial infarction; tissue rejection; transplantation; psoriasis;		
XX	autoimmune disease; multiple sclerosis; Mab.		
XX	Homo sapiens.		
XX	WO9845710-A1.		
XX	15-OCT-1998.		
XX	11-APR-1997;	97WO-US06500.	
XX	07-APR-1997;	97US-6667777.	
XX	(WEBB/) WEBBER R.		
XX	Webber R;		
XX	WPI; 1998-594495/50.		
XX	Detection of human inducible nitric oxide synthase - using an		
XX	immunoassay in which a sample is contacted with a specific binding		
XX	entity reactive with human iNOS or mimics.		
XX	Example 3; Page 32; 93pp; English.		
XX	This invention describes an immunoassay method where a sample with a		
XX	specific binding entity (e.g. a monoclonal antibody) reactive to human		
XX	inducible nitric oxide synthase (iNOS) or mimics of this protein is used		
XX	to detect the presence of human iNOS protein in the sample. The method		
XX	can be used for the detection and quantitation of human iNOS in cells and		
XX	tissues for various pathophysiological conditions such as sepsis, septic		
XX	shock, myocardial infarction, rejection of tissue in organs following		
XX	transplantation, monitoring "flare ups" in certain autoimmune diseases		
XX	such as lupus, psoriasis, and multiple sclerosis. This sequence		
XX	represents a peptide from human iNOS which is used in the method of the		
XX	invention.		
XX	Sequence	18 AA;	
XX	Query Match	100.0%; Score 96; DB 19; Length 18;	
XX	Best Local Similarity	100.0%; Pred. No. 1.le-09;	
XX	Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	SPVTQDDLQYHNLSKQQN 18	
Db	1	sptvqddllqyhnlskqgn 18	
RESULT	6		
AAW96322			
ID	AAW96322	standard; Protein; 1146 AA.	
XX	AAW96322;		
XX	28-JUN-1999	(first entry)	
XX	Inducible nitric oxide synthase.		
XX	Manganese containing superoxide dismutase; MnSOD; IDDM;		
XX	diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell;		
XX	fatty acid; lipotoxic; cytotoxic; cytokine; osteoporosis;		
XX	inflammatory disease; autoimmune disease; neurodegenerative disease.		
XX	Homo sapiens.		

PN WO9906059-A2.  
 XX 11-FEB-1999.  
 XX 30-JUL-1998; 98WO-US15781.  
 PF 03-MAR-1998; 98US-0055092.  
 PR 30-JUL-1997; 97US-0055092.  
 XX (BETA-) BETAGENE INC.  
 PA (TEXA) UNIV TEXAS SYSTEM.  
 XX Clark SA, Holmeyer H, Koyama K, Lee Y, Newgard CB;  
 PI Ohneda M, Shimabukuro, Thigpen A, Unger RH;  
 XX WPI; 1999-153448/13.  
 DR N-PSDB; AAX08434.  
 XX Protection of mammalian cells against immunotoxicity or lipotoxicity  
 PT - used for treating, e.g. diabetes, obesity, wasting syndromes,  
 PT osteoporosis, inflammatory diseases, autoimmune diseases or  
 PT neurodegenerative diseases  
 XX Disclosure; Page 247-251; 253pp; English.  
 PS Inhibition of cytokine mediated immunotoxicity of cells can be  
 CC achieved by blocking free radical production or the accumulation of  
 CC free radicals in that cell. Treatment of insulin dependent diabetes  
 CC mellitus (IDDM) can be achieved by blocking nitric oxide (NO)  
 CC production in a pancreatic beta cell and by providing a composition  
 CC comprising an agent that reduces levels of fatty acids in the cells  
 CC and protects beta-cells of the subject against lipid-mediated cell  
 CC death. Cells can also be protected against nitric oxide mediated  
 CC cytotoxicity by introducing into the cell an antioxidant agent.  
 CC The methods can be used for protecting cells against immunotoxicity  
 CC mediated by, e.g. IL-1 beta, IL-1 alpha, gamma IFN, TNF alpha, TNF  
 CC beta, IL-8, IL-2, IL-6, IL-3, IL-5, IL-9, IL-14, IL-17,  
 CC granulocyte-macrophage colony stimulating factor or monocyte  
 CC chemoattractant protein-1. The methods can be used for the treatment  
 CC of e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity,  
 CC wasting syndromes, short stature, osteoporosis, inflammatory  
 CC diseases, autoimmune diseases, or neurodegenerative diseases.  
 XX Sequence 1146 AA;  
 SQ

Query Match 100.0%; Score 96; DB 20; Length 1146;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVTQDDLOYHNLKQON 18  
 Db |||||

RESULT 7  
 AAR55764  
 ID AAR55764 standard; Protein; 1153 AA.  
 XX AAR55764;  
 XX 28-DEC-1994 (first entry)  
 DE Sequence encoded by the cDNA clone for human hepatocyte inducible  
 DE nitric oxide synthase.  
 XX Nitric oxide synthase; hepatocyte; hypotensive shock; therapy.  
 KW Homo sapiens.  
 OS  
 XX WO9412645-A.  
 PN 09-JUN-1994.

XX 23-NOV-1993; 93WO-US11401.  
 PF 25-NOV-1992; 92US-0981344.  
 XX (UVPI-) UNIV PITTSBURGH.  
 PA Billiar TR, Geller DA, Nussler AK, Simmons RL;  
 PI WPI; 1994-200273/24.  
 DR N-PSDB; AAQ66914.  
 XX cDNA clone encoding human inducible nitric oxide synthase - used  
 PT to prevent the hypotensive shock seen with sepsis.  
 PT Disclosure; Fig 1; 53pp; English.  
 PS AAQ66914 is from human hepatocyte inducible nitric oxide synthase cDNA  
 CC clone PHINOS from lambda zap II cDNA library. The original source  
 CC was induced human hepatocyte RNA. HINOS cDNA plasmid is pref.  
 CC transformed in E. coli SOLR (ATCC 69126). The inventors claim a  
 CC clone with the cDNA sequence in AAQ66914 and a cDNA clone which  
 CC encodes AAR55764. The cloning and expression of a human tissue nitric  
 CC oxide synthase cDNA provides a source of the enzyme for therapeutic  
 CC purposes, for example to prevent the hypotensive shock seen with  
 CC sepsis.  
 XX Sequence 1153 AA;  
 SQ

Query Match 100.0%; Score 96; DB 15; Length 1153;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVTQDDLOYHNLKQON 18  
 Db |||||

RESULT 8  
 AAR63206  
 ID AAR63206 standard; Protein; 1153 AA.  
 XX AAR63206;  
 XX 09-MAY-1995 (first entry)  
 DE Nitric-oxide-synthase.  
 XX Nitric-oxide-synthase; NO-synthase; NOS; chondrocyte;  
 KW interleukin-1-beta; PBHSINOS; arthritis; hypertension;  
 KW septic shock; inflammation; ischemia; dementia; obesity; tumor;  
 KW agonist; antagonist; vector; CHO; Chinese hamster ovary;  
 KW cell culture.  
 KW Homo sapiens.  
 OS  
 XX WO9423038-A.  
 PN 13-OCT-1994.  
 PD 25-MAR-1994; 94WO-GB00621.  
 XX 26-MAR-1993; 93GB-0006386.  
 PR (WELL) WELLCOME FOUND LTD.  
 XX Charles IG, Moncada SE, Palmer RMJ, Moncada S;  
 PI WPI; 1994-333198/41.  
 DR N-PSDB; AAQ77700.  
 XX New human inducible nitric oxide synthase - useful for  
 PT

PT Identifying enzyme inhibitors and stimulators, and for diagnosis  
 PT and treatment of e.g. viral infections or tumours

PS Disclosure; Page 25-31; 42pp; English.

XX Human chondrocytes were incubated with interleukin-1-beta to induce  
 CC nitric-oxide-synthase. cDNA was generated and used to construct a  
 CC library in lambda ZAPII. This was screened with a 650 bp fragment of  
 CC mouse inducible NO-synthase cDNA to identify the full-length clone  
 CC pBSHINOS. The insert was transferred to pSVL to give a vector  
 CC capable of expressing NO-synthase in CHO cells under control of a  
 CC heterologous constitutive promoter.

XX Sequence 1153 AA;

Query Match 100.0%; Score 96; DB 15; Length 1153;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVTQDDLOYHNLKQON 18

DB 37 spvtgddlqyhnlkskqgn 54

RESULT 9

AAR88464

ID AAR88464 standard; Protein; 1153 AA.

XX

AC AAR88464;

XX

DT 13-MAY-1996 (first entry)

XX

DE Hepatocyte inducible nitric oxide synthase.

XX

KW Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy;  
 KW vascular occlusive disease; cancer; infection.

XX

OS Homo sapiens.

XX

PN WO9600006-A1.

XX

PD 04-JAN-1996.

XX

PF 20-JUN-1995; 95WO-US07849.

XX

PR 24-JUN-1994; 94US-0265046.

XX

PA (UYPI-) UNIV PITTSBURGH.

XX

PI Billiar TR, Geller DA, Nussler AK, Simmons RL, Tzeng E;

XX

DR WPI; 1996-068641/07.

XX

DR N-PSDB; AAT10115.

XX

PT Inducible nitric oxide synthase gene - useful in gene therapy to

PT treat, e.g. vascular occlusive disease and cancer

XX

PS Disclosure; Page 54-58; 91pp; English.

XX

CC An inducible nitric oxide synthase (iNOS - AAR88464) is the product  
 CC of a cDNA clone (AAT10115) derived from human hepatocytes induced  
 CC for iNOS biosynthesis. The iNOS can be obtd. by expression of  
 CC the cDNA e.g. in mammalian host cells and is used in the  
 CC development of selective inhibitors of NOS or to treat diseases  
 CC affected by nitric oxide.

XX

SQ Sequence 1153 AA;

Query Match 100.0%; Score 96; DB 17; Length 1153;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVTQDDLOYHNLKQON 18

DB 37 spvtgddlqyhnlkskqgn 54

RESULT 10

AAW36113

ID AAW36113 standard; Protein; 1153 AA.

XX

AC AAW36113;

XX

DT 11-MAY-1998 (first entry)

XX

DE Human inducible nitric oxide synthetase.

XX

KW Nitric oxide synthetase; NOS; iNOS; HPIiNOS; human;

KW erectile dysfunction; impotence; gene therapy; corpora cavernosa;

KW relaxant.

XX

OS Homo sapiens.

XX

PN WO9742965-A1.

XX

PD 20-NOV-1997.

XX

PF 09-MAY-1997; 97WO-US07643.

XX

PR 10-MAY-1996; 96US-0017373.

XX

PA (GONZ/) GONZALEZ-CADAVID N F.

XX

PA (RAJF/) RAJFER J.

XX

PI Gonzalez-Cadavid NF, Rajfer J;

XX

DR WPI; 1998-008577/01.

DR

DR N-PSDB; AAT98199.

XX

PT Treatment of erectile dysfunction - by introducing an agent into

PT penile tissue, particularly for inducing cavernosal smooth muscle

PT relaxation or increasing NOS levels

XX

PS Claim 12; Page 38-41; 53pp; English.

XX

CC This protein comprises human penis inducible nitric oxide  
 CC synthetase (HPIiNOS). Its amino acid sequence was deduced from a  
 CC cDNA clone (see AAT98199) derived from human penile smooth muscle  
 CC cell mRNA. The invention is directed to a method of treating  
 CC erectile dysfunction in a patient by providing an agent capable of  
 CC treating erectile dysfunction, and introducing an effective amount  
 CC of the agent into the penile tissue of the patient. Preferably,  
 CC the agent induces cavernosal smooth muscle relaxation, and/or  
 CC produces an increase in the level of NOS in tissue. Preferably,  
 CC the NOS is iNOS, and the agent is introduced into the corpora  
 CC cavernosa of the penis. The agent is preferably an NOS inducer, an  
 CC NOS protein such as HPIiNOS, a cDNA encoding an NOS such as HPIiNOS,  
 CC or cDNA transformed penile cells, especially corpora cavernosa  
 CC cells.

SQ Sequence 1153 AA;

Query Match

Best Local Similarity 100.0%; Score 96; DB 19; Length 1153;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVTQDDLOYHNLKQON 18

DB 37 spvtgddlqyhnlkskqgn 54

RESULT 11

AAB31724

ID AAB31724 standard; Protein; 1153 AA.  
XX  
AC AAB31724;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Amino acid sequence of a human inducible nitric oxide synthase (NOS).  
XX  
KW Gene therapy; angiogenesis; nucleic acid delivery; arteriosclerosis;  
KW nitric oxide synthase; NOS; endothelial dysfunction.  
XX  
OS Homo sapiens.  
XX  
PN WO200103728-A2.  
XX  
PD 18-JAN-2001.  
XX  
PF 07-JUL-2000; 2000WO-NL00482.  
XX  
PR 09-JUL-1999; 99EP-0202263.  
XX  
PR 09-JUL-1999; 99US-0143101.  
XX  
PA (INTR-) INTROGENE BV.  
XX  
PI Vogels R, Verlinden SFF;  
XX  
DR WPI; 2001-123142/13.  
XX  
PT Nucleic acid delivery vehicle comprising a nucleic acid encoding nitric  
PT oxide synthase, used for isolated tissue perfusion treatment to enhance  
PT and induce angiogenesis -  
XX  
PS Disclosure; Fig 6; 37pp; English.  
XX  
CC The specification describes a method for gene therapy for enhancing  
CC and inducing angiogenesis. The method uses a nucleic acid delivery  
CC vehicle, which comprises a nucleic acid encoding nitric oxide synthase  
CC (NOS). The delivery vehicle is used for the manufacture of a  
CC pharmaceutical composition for isolated tissue perfusion treatment.  
CC The method is useful for enhancing and/or inducing angiogenesis in  
CC patients with endothelial dysfunctions, in particular arteriosclerosis.  
CC The present sequence represents an inducible NOS.  
XX  
SQ Sequence 1153 AA;  
  
Query Match 100.0%; Score 96; DB 22; Length 1153;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SPVTODDLQYHNLSKQON 18  
Db 37 spvtqddlqyhnlskqgn 54  
  
RESULT 12  
AAB66724  
ID AAB66724 standard; protein; 1153 AA.  
XX  
AC AAB66724;  
XX  
DT 09-APR-2001 (first entry)  
XX  
DE Human inducible nitric oxide synthase.  
XX  
KW Nitric oxide synthase; NOS; angiogenesis; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN EP1067190-A1.  
XX  
PD 10-JAN-2001.  
XX

PF 09-JUL-1999; 99EP-0202263.  
XX  
PR 09-JUL-1999; 99EP-0202263.  
XX  
PA (INTR-) INTROGENE BV.  
XX  
PI Vogels R, Verlinden S;  
XX  
DR WPI; 2001-125729/14.  
XX  
PT Use of a nucleic acid delivery vehicle comprising a nucleic acid  
PT encoding nitric oxide synthase, especially useful in gene therapy for  
PT enhancing and/or inducing angiogenesis and treating atherosclerosis -  
XX  
PS Examples; Page 14-18; 39pp; English.  
XX  
CC The present invention relates to use of a nucleic acid delivery  
CC vehicle comprising a nucleic acid encoding nitric oxide synthase  
CC (NOS) activity for the manufacture of a composition for essentially  
CC isolated tissue perfusion treatment to enhance and/or induce  
CC angiogenesis. The nucleic acid delivery vehicle is particularly  
CC useful in gene therapy for the treatment of atherosclerosis.  
XX  
SQ Sequence 1153 AA;  
  
Query Match 100.0%; Score 96; DB 22; Length 1153;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SPVTODDLQYHNLSKQON 18  
Db 37 spvtqddlqyhnlskqgn 54  
  
RESULT 13  
AAW81223  
ID AAW81223 standard; peptide; 15 AA.  
XX  
AC AAW81223;  
XX  
DT 30-APR-1999 (first entry)  
XX  
DE Human iNOS peptide fragment PS-5261.  
XX  
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 15 /note= "Asn residue amidated"  
FT  
XX  
PN WO9845710-A1.  
XX  
PD 15-OCT-1998.  
XX  
PF 11-APR-1997; 97WO-US06500.  
XX  
PR 07-APR-1997; 97US-6667777.  
XX  
PA (WEBB/) WEBBER R.  
XX  
PI Webber R;  
XX  
DR WPI; 1998-594495/50.  
XX  
PT Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
XX

XX Example 4; Page 35; 93pp; English.

XX This invention describes an immunoassay method where a sample with a

CC specific binding entity (e.g. a monoclonal antibody) reactive to human

CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used

CC to detect the presence of human iNOS protein in the sample. The method

CC can be used for the detection and quantitation of human iNOS in cells and

CC tissues for various pathophysiological conditions such as sepsis, septic

CC shock, myocardial infarction, rejection of tissue in organs following

CC transplantation, monitoring "flare ups" in certain autoimmune diseases

CC such as lupus, psoriasis, and multiple sclerosis. This sequence

CC represents a peptide from human iNOS which is used in the method of the

CC invention.

XX Sequence 15 AA;

Query Match 84.4%; Score 81; DB 19; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.8e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TQDDQYHNLKSKQN 18

DB 1 tqddqyhnlkskqn 15

RESULT 14

AAW81288

ID AAW81288 standard; peptide; 15 AA.

AC AAW81288;

XX 30-APR-1999 (first entry)

XX Human iNOS peptide fragment for epitope mapping #9.

XX Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;

KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;

KW myocardial infarction; tissue rejection; transplantation; psoriasis;

KW autoimmune disease; multiple sclerosis; epitope mapping.

XX Homo sapiens.

XX WO9845710-A1.

XX 15-OCT-1998.

XX 11-APR-1997; 97WO-US06500.

XX 07-APR-1997; 97US-666777.

XX (WEBB/) WEBBER R.

XX Webber R;

XX WPI; 1998-594495/50.

XX Detection of human inducible nitric oxide synthase - using an

PT immunoassay in which a sample is contacted with a specific binding

PT entity reactive with human iNOS or mimics.

XX Example 4; Fig 7A; 93pp; English.

XX This invention describes an immunoassay method where a sample with a

CC specific binding entity (e.g. a monoclonal antibody) reactive to human

CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used

CC to detect the presence of human iNOS protein in the sample. The method

CC can be used for the detection and quantitation of human iNOS in cells and

CC tissues for various pathophysiological conditions such as sepsis, septic

CC shock, myocardial infarction, rejection of tissue in organs following

CC transplantation, monitoring "flare ups" in certain autoimmune diseases

CC such as lupus, psoriasis, and multiple sclerosis. This sequence

CC represents a peptide from human iNOS which is used in the method of the

CC invention.

XX Sequence 15 AA;

Query Match 84.4%; Score 81; DB 19; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.8e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TQDDQYHNLKSKQN 18

DB 1 tqddqyhnlkskqn 15

RESULT 15

AAW81263

ID AAW81263 standard; peptide; 17 AA.

XX AC AAW81263;

XX 30-APR-1999 (first entry)

XX Human iNOS peptide fragment PS-5104.

XX Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;

KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;

KW myocardial infarction; tissue rejection; transplantation; psoriasis;

KW autoimmune disease; multiple sclerosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 17

FT /note= "Asn residue amidated"

XX WO9845710-A1.

XX 15-OCT-1998.

XX 11-APR-1997; 97WO-US06500.

XX 07-APR-1997; 97US-666777.

XX (WEBB/) WEBBER R.

XX Webber R;

XX WPI; 1998-594495/50.

XX Detection of human inducible nitric oxide synthase - using an

PT immunoassay in which a sample is contacted with a specific binding

PT entity reactive with human iNOS or mimics.

XX Example 12; Page 52; 93pp; English.

XX This invention describes an immunoassay method where a sample with a

CC specific binding entity (e.g. a monoclonal antibody) reactive to human

CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used

CC to detect the presence of human iNOS protein in the sample. The method

CC can be used for the detection and quantitation of human iNOS in cells and

CC tissues for various pathophysiological conditions such as sepsis, septic

CC shock, myocardial infarction, rejection of tissue in organs following

CC transplantation, monitoring "flare ups" in certain autoimmune diseases

CC such as lupus, psoriasis, and multiple sclerosis. This sequence

CC represents a peptide from human iNOS which is used in the method of the

CC invention.

XX Sequence 17 AA;

Query Match 83.9%; Score 80.5; DB 19; Length 17;

Best Local Similarity 94.4%; Pred. No. 4e-07;

Matches	17;	Conservative	0;	Mismatches	0;	Indels	1;	Gaps	1;
Qy	1	SPVTQDDLQYHNLSKQON	18						
Db	1	spvtqddl-yhnlskqgn	17						

Search completed: September 10, 2001, 14:00:24  
Job time: 168 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:11:12 ; Search time 72.54 Seconds  
(without alignments)  
32.830 Million cell updates/sec

Title: US-08-833-506c-30

Perfect score: 95

Sequence: 1 PALVQGLERVDGPTPH 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL16.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_unclassified.\*  
13: sp\_vertebrate.\*  
14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	165	4 Q9UD42	Q9ud42 homo sapien
2	95	100.0	1114	4 Q94994	Q94994 homo sapien
3	90	94.7	945	6 Q9N175	Q9n175 ovis aries
4	82	86.3	137	6 Q9N2C9	Q9n2c9 equus caball
5	77	81.1	649	6 Q9XT88	Q9xt88 canis famil
6	60	63.2	1154	6 Q97604	Q97604 canis famil
7	59	62.1	1147	11 Q9QW28	Q9qw28 rattus sp.
8	55	57.9	1147	11 Q9R0W4	Q9r0w4 rattus norv
9	47	49.5	366	6 Q9N176	Q9n176 ovis aries
10	47	49.5	386	10 Q9ZPW1	Q9zpw1 arabidopsis
11	47	49.5	748	2 Q9S522	Q9s522 lactococcus
12	47	49.5	842	2 Q69336	Q69336 streptomyce
13	47	49.5	1205	6 Q9TUX8	Q9tux8 canis famil
14	47	49.5	1206	11 Q9WTX6	Q9wtx6 cavia porce
15	46.5	48.9	100	2 Q9FBQ6	Q9fbq6 streptomyce
16	46	48.4	197	2 Q44568	Q44568 acetobacter
17	46	48.4	741	2 Q9RWS7	Q9rws7 deinococcus
18	46	48.4	758	2 Q9I0L8	Q9i0l8 pseudomonas
19	46	48.4	791	2 Q9X1B1	Q9x1b1 thermotoga

20	46	48.4	857	2 Q9KHC1	Q9khc1 secondary e
21	46	48.4	859	2 Q9JYQ8	Q9jyq8 neisseria m
22	46	48.4	859	2 Q9JTP9	Q9jtp9 neisseria m
23	46	48.4	861	2 Q9PGC1	Q9pgc1 xylella fas
24	46	48.4	954	14 Q66764	Q66764 encephalomy
25	46	48.4	2292	14 Q89272	Q89272 encephalomy
26	46	48.4	2292	14 Q66763	Q66763 encephalomy
27	46	48.4	2292	14 Q66765	Q66765 encephalomy
28	46	48.4	2292	14 Q66850	Q66850 encephalomy
29	46	48.4	2292	14 Q83422	Q83422 mengo encep
30	45	47.4	816	2 Q9ZIL9	Q9zil9 lactococcus
31	45	47.4	854	2 Q9HVN5	Q9hvn5 pseudomonas
32	45	47.4	1555	5 Q9NMZ9	Q9nmz9 leishmania
33	44	46.3	143	2 Q9FD20	Q9fd20 streptomyce
34	44	46.3	152	2 Q9F8K2	Q9f8k2 carboxydoth
35	44	46.3	508	2 P74942	P74942 thermus aqu
36	44	46.3	533	2 Q67741	Q67741 aquifex aeo
37	44	46.3	854	2 Q9RA63	Q9rac3 thermus aqu
38	44	46.3	911	10 Q9LE57	Q9le57 arabidopsis
39	44	46.3	983	2 Q9HV74	Q9hv74 pseudomonas
40	44	46.3	1024	4 Q9ULE3	Q9ule3 homo sapien
41	43	45.3	80	2 Q9HW44	Q9hw44 pseudomonas
42	43	45.3	200	2 Q07124	Q07124 lactobacill
43	43	45.3	322	2 Q88063	Q88063 streptomyce
44	43	45.3	379	1 Q9VIM1	Q9v1m1 pyrococcus
45	43	45.3	407	2 Q34413	Q34413 bacillus su

## ALIGNMENTS

RESULT 1

Q9UD42 ID Q9UD42 PRELIMINARY; PRT; 165 AA.  
AC Q9UD42;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE NITRIC OXIDE SYNTHASE, NOS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-95096875; PubMed-7528267;  
RA Fujisawa H., Ogura T., Hokari A., Weisz A., Yamashita J., Esumi H.;  
RT "Inducible nitric oxide synthase in a human glioblastoma cell line.";  
RL J. Neurochem. 64:85-91(1995).  
DR InterPro; IPR003097; -;  
DR Pfam; PF00667; FAD\_binding; 1.  
SQ SEQUENCE 165 AA; 18466 MW; 99626E5FD04C2C3D CRC64;

Query Match 100.0%; Score 95; DB 4; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVQGLERVDGPTPH 18

Db 115 PALVQGLERVDGPTPH 132

RESULT 2

Q94994 ID Q94994 PRELIMINARY; PRT; 1114 AA.  
AC Q94994;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE INDUCIBLE NITRIC OXIDE SYNTHASE.  
OS INOS.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ogawa Y., Nishijima S., Goto M., Ida M.;  
 RT "Cloning and characterization of a novel splice variant of human  
 RT inducible nitric oxide synthase.";  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB022318; BAA37123.1; -;  
 DR HSSP; P35228; 4NOS.  
 DR InterPro; IPR001094; -;  
 DR InterPro; IPR001433; -;  
 DR InterPro; IPR001709; -;  
 DR InterPro; IPR003097; -;  
 DR Pfam; PF00175; oxidored\_fad; 1.  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 SQ SEQUENCE 1114 AA; 126748 MW; CLF9624774435571 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 1114;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVQGILERVVDGPTPH 18

|||||

DB 742 PALVQGILERVVDGPTPH 759

RESULT 3  
 QN175  
 ID Q9N175 PRELIMINARY; PRT; 945 AA.  
 AC Q9N175;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE INDUCIBLE NITRIC OXIDE SYNTHASE (FRAGMENT).  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mershon J.L., Clark K.E.;  
 RT "Estrogen increases the expression of iNOS in the ovine coronary  
 RT artery.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF223942; RAF34710.1; -;  
 DR InterPro; IPR001094; -;  
 DR InterPro; IPR001433; -;  
 DR InterPro; IPR001709; -;  
 DR InterPro; IPR003097; -;  
 DR Pfam; PF00175; oxidored\_fad; 1.  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 FT NON\_TER 1 1  
 FT NON\_TER 945 945  
 SQ SEQUENCE 945 AA; 108001 MW; 9A5ACFD40440A74F CRC64;

Query Match 94.7%; Score 90; DB 6; Length 945;  
 Best Local Similarity 94.4%; Pred. No. 6.9e-06;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PALVQGILERVVDGPTPH 18

|||||

DB 605 PALVQGILERVVDGPTPH 622

RESULT 4  
 QN2C9  
 ID Q9N2C9 PRELIMINARY; PRT; 137 AA.  
 AC Q9N2C9;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE INDUCIBLE NITRIC OXIDE SYNTHASE (FRAGMENT).  
 GN INOS.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=THOROUGHbred; TISSUE=ARTERIAL ENDOTHELIIUM;  
 RA Ishida N., Sato F., Hasegawa T.;  
 RT "Molecular cloning of equine inducible NO synthase mRNA.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB039864; BAA92428.1; -;  
 DR InterPro; IPR003097; -;  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR NON\_TER 1 1  
 FT NON\_TER 137 137  
 SQ SEQUENCE 137 AA; 15429 MW; 50CCF954A814B64A CRC64;

Query Match 86.3%; Score 82; DB 6; Length 137;  
 Best Local Similarity 94.1%; Pred. No. 1.5e-05;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PALVQGILERVVDGPTP 17

|||||

DB 31 PALVQGILERVVDGPAP 47

RESULT 5  
 QN288  
 ID Q9N288 PRELIMINARY; PRT; 649 AA.  
 AC Q9N288;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE INDUCIBLE NITRIC OXIDE SYNTHASE (FRAGMENT).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLENIC VEIN;  
 RA Fulton D., Papapetropoulos A., Zhang X., Catravas J.D., Hintze T.H.,  
 RA Sessa W.C.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF068682; AAD39341.1; -;  
 DR HSSP; P35228; INST.  
 DR InterPro; IPR001094; -;  
 DR InterPro; IPR003097; -;  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 FT NON\_TER 1 1  
 FT NON\_TER 649 649  
 SQ SEQUENCE 649 AA; 74304 MW; A645F80FFA9DBFB7 CRC64;

Query Match 81.1%; Score 77; DB 6; Length 649;  
 Best Local Similarity 88.2%; Pred. No. 0.00055;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALVQGILERVVDGPTPH 18

|||||

DB 610 ALVQGILERVVDSPAPH 626

```

RESULT 6
O97604 PRELIMINARY; PRT: 1154 AA.
AC O97604;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE INDUCIBLE NITRIC OXIDE SYNTHASE.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=AORTA;
RX MEDLINE=98431941; PubMed=9746458;
RA Wang X., McGregor C.G.A., Miller V.M.;
RT "Induction and cDNA sequence of inducible nitric oxide synthase from
RT canine aortic smooth muscle cells.";
RL Am. J. Physiol. 275:H1122-H1129(1998).
DR EMBL; AF077821; AAC78630.1; -
DR HSSP; P29477; INOS.
DR InterPro; IPR001094; -
DR InterPro; IPR001433; -
DR InterPro; IPR001709; -
DR InterPro; IPR003097; -
DR Pfam; PF00175; oxidoreduced_fad; 1.
DR Pfam; PF00667; FAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
SQ SEQUENCE 1154 AA; 131709 MW; 42CD606E447254CB CRC64;

Query Match 63.2%; Score 60; DB 6; Length 1154;
Best Local Similarity 81.2%; Pred. No. 0.56;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ALVQGLERVVVDGTP 17
| | | | | | | | | | | | | | | | | |
DB 779 ALVQGLERVVVSPAP 794

RESULT 7
O9QW28 PRELIMINARY; PRT: 1147 AA.
AC O9QW28;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE CYTOKINE INDUCIBLE NITRIC OXIDE SYNTHASE, INOS.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93221515; PubMed=7682072;
RA Wood E.R., Berger H.Jr., Sherman P.A., Lapetina E.G.;
RT "Hepatocytes and macrophages express an identical cytokine inducible
RT nitric oxide synthase gene.";
RL Biochem. Biophys. Res. Commun. 191:767-774(1993).
DR HSSP; P29477; INOS.
DR InterPro; IPR001094; -
DR InterPro; IPR001433; -
DR InterPro; IPR001709; -
DR InterPro; IPR002369; -
DR InterPro; IPR003097; -
DR Pfam; PF00175; oxidoreduced_fad; 1.
DR Pfam; PF00667; FAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR ProDom; PD001811; -; 1.

```

```

SQ SEQUENCE 1147 AA; 130625 MW; 2CAF8983E56F651A CRC64;

Query Match 62.1%; Score 59; DB 11; Length 1147;
Best Local Similarity 81.2%; Pred. No. 0.81;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALVQGLERVVVDGTP 17
| | | | | | | | | | | | | | | | | |
DB 779 ALVQGLERVVDCSSP 794

RESULT 8
O9ROW4 PRELIMINARY; PRT: 1147 AA.
AC O9ROW4;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE INDUCIBLE NITRIC OXIDE SYNTHASE.
OS INOS.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=WISTAR KYOTO;
RX MEDLINE=99326503; PubMed=10395902;
RA Keinänen R.A., Vartiainen N., Koistinaho J.;
RT "Molecular cloning and characterization of the rat inducible nitric
RT oxide synthase (iNOS) gene.";
RL Gene 234:297-305(1999).
DR EMBL; AJ230462; CAB46089.1; -
DR EMBL; AJ230463; CAB46089.1; JOINED.
DR EMBL; AJ230464; CAB46089.1; JOINED.
DR EMBL; AJ230465; CAB46089.1; JOINED.
DR EMBL; AJ230466; CAB46089.1; JOINED.
DR EMBL; AJ230467; CAB46089.1; JOINED.
DR EMBL; AJ230468; CAB46089.1; JOINED.
DR EMBL; AJ230469; CAB46089.1; JOINED.
DR EMBL; AJ230470; CAB46089.1; JOINED.
DR EMBL; AJ230471; CAB46089.1; JOINED.
DR EMBL; AJ230472; CAB46089.1; JOINED.
DR EMBL; AJ230473; CAB46089.1; JOINED.
DR EMBL; AJ230474; CAB46089.1; JOINED.
DR EMBL; AJ230475; CAB46089.1; JOINED.
DR EMBL; AJ230476; CAB46089.1; JOINED.
DR EMBL; AJ230477; CAB46089.1; JOINED.
DR EMBL; AJ230478; CAB46089.1; JOINED.
DR EMBL; AJ230479; CAB46089.1; JOINED.
DR EMBL; AJ230480; CAB46089.1; JOINED.
DR EMBL; AJ230481; CAB46089.1; JOINED.
DR EMBL; AJ230482; CAB46089.1; JOINED.
DR EMBL; AJ230483; CAB46089.1; JOINED.
DR EMBL; AJ230484; CAB46089.1; JOINED.
DR EMBL; AJ230485; CAB46089.1; JOINED.
DR EMBL; AJ230486; CAB46089.1; JOINED.
DR EMBL; AJ230487; CAB46089.1; JOINED.
DR HSSP; P29477; INOS.
DR InterPro; IPR001094; -
DR InterPro; IPR001433; -
DR InterPro; IPR001709; -
DR InterPro; IPR003097; -
DR Pfam; PF00175; oxidoreduced_fad; 1.
DR Pfam; PF00667; FAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
SQ SEQUENCE 1147 AA; 130613 MW; E76B3F8407D54CF6 CRC64;

Query Match 57.9%; Score 55; DB 11; Length 1147;
Best Local Similarity 80.0%; Pred. No. 3.6;

```

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVQGILERVVDGTPP 17  
|||||  
Db 780 LVQGILERVVDCCSP 794

RESULT 9  
Q9N176 PRELIMINARY; PRT; 366 AA.  
ID Q9N176  
AC Q9N176;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE ENDOTHELIAL NITRIC OXIDE SYNTHASE (FRAGMENT).  
GN 23B.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID:9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Merzhon J.L., Clark K.E.;  
RT "Estrogen increases the expression of iNOS in the ovine coronary  
artery."  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF223471; AAF34707.1; -;  
DR InterPro; IPR001433; -;  
DR InterPro; IPR001709; -;  
DR InterPro; IPR003097; -;  
DR Pfam; PF00175; oxidored\_fad; 1.  
DR Pfam; PF00667; FAD\_binding; 1.  
DR PRINTS; PR00371; FPNCR.  
DR NON\_TER 1  
FT NON\_TER 366  
SQ SEQUENCE 366 AA; 40791 MW; 794B274DA786A4A0 CRC64;

Query Match 49.5%; Score 47; DB 6; Length 366;  
Best Local Similarity 52.9%; Pred. No. 19;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PALVQGILERVVDGTPP 17  
| |||: || || || || ||  
Db 54 PGLVEALLSRVEDPPPP 70

RESULT 10  
Q92PW1 PRELIMINARY; PRT; 386 AA.  
ID Q92PW1  
AC Q92PW1;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE PUTATIVE TUBBY PROTEIN.  
GN T30D6.21.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsiis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,  
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.,  
RA Carrara A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,  
RA Fraser C.M., Venter J.C.;  
RT "Arabidopsis thaliana chromosome II BAC T30D6 genomic sequence."  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC006439; AAD15508.1; -;  
DR HSSP; P50586; 1C8Z.

DR InterPro; IPR000007; -;  
DR Pfam; PF01167; Tub; 1.  
DR PROSITE; PS01200; TUB\_1; UNKNOWN\_1.  
DR PROSITE; PS01201; TUB\_2; UNKNOWN\_1.  
SQ SEQUENCE 386 AA; 43092 MW; 65BB8DE7851237FA CRC64;

Query Match 49.5%; Score 47; DB 10; Length 386;  
Best Local Similarity 52.9%; Pred. No. 20;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 PALVQGILERVVDGTPP 17  
|:||||| | | | |  
Db 254 PSVQGIIEEVSSSPSP 270

RESULT 11  
Q9S522 PRELIMINARY; PRT; 748 AA.  
ID Q9S522  
AC Q9S522;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE CLPE.  
GN CLPE.  
OS Lactococcus lactis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
OC Lactococcus.  
OX NCBI\_TaxID=1358;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MG1363;  
RX MEDLINE=99194715; PubMed=10094684;  
RA Ingmer H., Vogensen F.K., Hammer K., Kilstrup M.;  
RT "Disruption and analysis of the clpB, clpC, and clpE genes in  
RT Lactococcus lactis: ClpE, a new Clp family in gram-positive  
RT bacteria."  
RL J. Bacteriol. 181:2075-2083(1999).  
DR EMBL; AF023421; AAD01782.1; -;  
DR InterPro; IPR001270; -;  
DR InterPro; IPR001939; -;  
DR InterPro; IPR001943; -;  
DR InterPro; IPR003593; -;  
DR Pfam; PF00004; AAA; 2.  
DR Pfam; PF02151; UVR; 1.  
DR PRINTS; PR00300; CLPPROTEASEA.  
DR PROSITE; PS00870; CLPAB\_1; 1.  
DR PROSITE; PS00871; CLPAB\_2; 1.  
DR SMART; SM00382; AAA; 1.  
SQ SEQUENCE 748 AA; 83265 MW; E9E87F932E4A5C4A CRC64;

Query Match 49.5%; Score 47; DB 2; Length 748;  
Best Local Similarity 43.8%; Pred. No. 42;  
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 ALVQGILERVVDGTPP 17  
|:|:|:|:|:|:| |  
Db 160 AVVEGLAQIVDGVDP 175

RESULT 12  
O69936 PRELIMINARY; PRT; 842 AA.  
ID O69936  
AC O69936;  
DT 01-AUG-1998 (TREMBLrel. 07, Created)  
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE CLP PROTEASE ATP BINDING SUBUNIT.  
GN CLPA.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycetaceae; Streptomyces.

OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Oliver K., Harris D.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RX MEDLINE=97000351; PubMed=8843436;  
RA Redenbach M., Kieser H.M., Denapait D., Eichner A., Cullum J.,  
RA Kinashi H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for  
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RL Mol. Microbiol. 21:77-96(1996).  
DR EMBL; AL023861; CAA19619.1; -;  
DR InterPro; IPR001270; -;  
DR InterPro; IPR001939; -;  
DR InterPro; IPR001943; -;  
DR InterPro; IPR003593; -;  
DR Pfam; PF00004; AAA; 2;  
DR Pfam; PF02151; UVR; 1;  
DR PRINTS; PR00300; CLPPROTEASEA.  
DR PROSITE; PS00870; CLPAB.1; 1;  
DR PROSITE; PS00871; CLPAB.2; 1;  
DR SMART; SM00382; AAA; 1;  
KW Protease.  
SQ SEQUENCE 842 AA; 92110 MW; A8ADC12FDA90197F CRC64;

Query Match 49.5%; Score 47; DB 2; Length 842;  
Best Local Similarity 43.8%; Pred. No. 48;  
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 ALVQGILERVVDGTP 17  
|:|:|:|:|:|:|  
Db 243 AIVEGLAQRITGDVDP 258

RESULT 13  
Q9TUX8 PRELIMINARY; PRT; 1205 AA.  
AC Q9TUX8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE NITRIC OXIDE SYNTHASE.  
GN NOS.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEART;  
RX MEDLINE=99369487; PubMed=10442857;  
RA Schwemmer M., Bassege E.;  
RT "Assembly and characterization of canine heart endothelial nitric  
oxide synthase cDNA and 5'-flanking sequence by homology (RT-)PCR  
cloning.";  
RL Nitric Oxide 3:254-264(1999).  
DR EMBL; AF145503; AAD52161.1; -;  
DR HSSP; P29474; 3NOS.  
DR InterPro; IPR001094; -;  
DR InterPro; IPR001433; -;  
DR InterPro; IPR001709; -;  
DR Pfam; PF00175; oxidore\_d; 1.  
DR

DR Pfam; PF00667; FAD\_binding; 1.  
DR PRINTS; PR00369; FLAVODOXIN.  
DR PRINTS; PR00371; FPNCR.  
SQ SEQUENCE 1205 AA; 133045 MW; C150CDEB01685BA5 CRC64;

Query Match 49.5%; Score 47; DB 6; Length 1205;  
Best Local Similarity 52.9%; Pred. No. 72;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 PALVQGILERVVDGTP 17  
|:|:|:|:|:|:|  
Db 809 PGLVEALLSRVEDPPPP 825

RESULT 14  
Q9WTK6 PRELIMINARY; PRT; 1206 AA.  
AC Q9WTK6;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE ENDOTHELIAL NITRIC OXIDE SYNTHASE.  
GN NOS3.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Derst C., Preisig-Mueller R., Rajan S., Daut J.;  
RT "Cloning and sequencing of guinea pig NO synthases.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF146041; AAD29753.1; -;  
DR EMBL; AF146040; AAD29752.1; -;  
DR HSSP; P29474; 3NOS.  
DR InterPro; IPR001094; -;  
DR InterPro; IPR001433; -;  
DR InterPro; IPR001709; -;  
DR InterPro; IPR003097; -;  
DR Pfam; PF00175; oxidore\_d; 1.  
DR Pfam; PF00667; FAD\_binding; 1.  
DR PRINTS; PR00369; FLAVODOXIN.  
DR PRINTS; PR00371; FPNCR.  
SQ SEQUENCE 1206 AA; 133692 MW; EB4E792D3F9503DD CRC64;

Query Match 49.5%; Score 47; DB 11; Length 1206;  
Best Local Similarity 52.9%; Pred. No. 72;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 PALVQGILERVVDGTP 17  
|:|:|:|:|:|:|  
Db 810 PGLVEALLSRVEDPPPP 826

RESULT 15  
Q9FBQ6 PRELIMINARY; PRT; 100 AA.  
AC Q9FBQ6;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE AMINOGLYCOSIDE PHOSPHOTRANSFERASE (FRAGMENT).  
GN SCD86A.01C.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Harris D.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RX MEDLINE-97000351; PubMed-8843436;  
 RA Redenbach M., Kleser H.W., Denapaita D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for  
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
 RL Mol. Microbiol. 21:77-96(1996).  
 DR EMBL; AL391541; CAC04254.1; -.  
 KW Transferase.  
 FT NON\_TER 100 100  
 SQ SEQUENCE 100 AA; 10559 MW; 2AE37FE5F3976A79 CRC64;

Query Match 48.9%; Score 46.5; DB 2; Length 100;  
 Best Local Similarity 52.4%; Pred. No. 5.3;  
 Matches 11; Conservative 2; Mismatches 5; Indels 3; Gaps 1;  
 QY 1 PALVOGILER---VVDGTPH 18  
 Db 25 PALAGFLERWELRDGPSMH 45

Search completed: September 10, 2001, 14:11:13  
 Job time: 592 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:09:52 ; Search time 23.82 Seconds  
(without alignments)  
25.886 Million cell updates/sec

Title: US-08-833-506c-30

Perfect score: 95

Sequence: 1 PALVQGLERVRVDGPTPH 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	1153	1 NS2A_HUMAN	P35228 homo sapien
2	79	83.2	1144	1 NOS2_MOUSE	P29477 mus musculu
3	74	77.9	1149	1 NOS2_CAVPO	O54705 cavia porce
4	59	62.1	1147	1 NOS2_RAT	O06518 rattus norv
5	59	62.1	1147	1 NOS2D_HUMAN	O60591 homo sapien
6	55	57.9	496	1 NOS2D_RABIT	O19114 oryctolaqu
7	49	51.6	1217	1 YHCR_BACSU	P54602 bacillus su
8	48	50.5	1202	1 NOS3_HUMAN	P29473 bos taurus
9	47	49.5	1204	1 NOS3_BOVIN	P29473 bos taurus
10	46	48.4	856	1 CLPB_HAEN	P44403 haemophilu
11	46	48.4	2290	1 POLG-EMCV	P03304 encephalomy
12	46	48.4	2292	1 POLG-EMCVB	P17593 encephalomy
13	46	48.4	2292	1 POLG-EMCVD	P17594 encephalomy
14	45.5	47.9	369	1 MURB_MYCTU	Q11148 mycobacteri
15	45	47.4	857	1 CLPB_ECOLI	P03815 escherichia
16	44	46.3	911	1 H101_ARATH	P42730 arabidopsis
17	43	45.3	637	1 YHES_ECOLI	P45535 escherichia
18	43	45.3	848	1 CLPB_MYCTU	O53719 mycobacteri
19	43	45.3	878	1 CLPB-TREPA	O83110 treponema p
20	43	45.3	908	1 H104_YEAST	P31539 saccharomyc
21	43	45.3	1136	1 NOS2_CHICK	O90703 gallus gall
22	43	45.3	1165	1 PEX6_PICPA	P33289 pichia past
23	42	44.2	763	1 CLPL_LACIA	O06716 lactococcus
24	42	44.2	811	1 HSP7_YEAST	P33416 saccharomyc
25	41	43.2	333	1 PEPR_LACDL	Q48544 lactobacill
26	41	43.2	467	1 INVO_MOUSE	P48997 mus musculu
27	41	43.2	504	1 DCMC_ANSAN	P12617 anser anser
28	41	43.2	530	1 HNA2_ARATH	P49294 arabidopsis
29	41	43.2	852	1 CLPB-CORGL	P53532 corynebacte
30	41	43.2	868	1 CLPB_TRYBB	P31543 trypanosoma
31	41	43.2	883	1 CLPB_SYNP7	P53533 synecococc
32	41	43.2	919	1 NOS3_RAT	O62600 rattus norv
33	41	43.2	1201	1 NOS3_MOUSE	P70313 mus musculu

34	40	42.1	277	1 ANGL_EWENI	Q00746 emericella
35	40	42.1	519	1 ACHG_MOUSE	P04760 mus musculu
36	40	42.1	519	1 ACHG_RAT	P18916 rattus norv
37	40	42.1	564	1 RK_RAT	Q63651 rattus norv
38	40	42.1	1001	1 TP3A_HUMAN	Q13472 homo sapien
39	40	42.1	1109	1 POL_CAEVC	P33459 caprine art
40	39.5	41.6	827	1 PTF1_RHOCA	P23388 r multiphos
41	39.5	41.6	2504	1 FAS_HUMAN	P49327 homo sapien
42	39.5	41.6	2505	1 FAS_RAT	P12785 rattus norv
43	39	41.1	218	1 VGLL_HSVB	P28941 equine herp
44	39	41.1	267	1 ELNE_HUMAN	P08246 homo sapien
45	39	41.1	584	1 MKS1_YEAST	P34072 saccharomyc

## ALIGNMENTS

RESULT	1
NS2A_HUMAN	
ID	NS2A_HUMAN STANDARD; PRT: 1153 AA.
AC	P35228; Q16692; O60757; Q16263;
DT	01-FEB-1994 (Rel. 28, Created)
DT	01-FEB-1996 (Rel. 33, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
DE	(INDUCIBLE NOS) (INOS) (HEPATOCYTE NOS) (HEP-NOS).
GN	NOS2A OR NOS2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RX	MEDLINE=93234523; PubMed=7682706;
RA	Geller D.A., Lowenstein C.J., Shapiro R.A., Nussler A.K.,
RA	di Silvio M., Wang S.C., Nakayama D.K., Simmons R.L., Snyder S.H.,
RA	Billiar T.R.;
RT	"Molecular cloning and expression of inducible nitric oxide synthase
RT	from human hepatocytes.";
RL	Proc. Natl. Acad. Sci. U.S.A. 90:3491-3495(1993).
RL	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Colorectal adenocarcinoma;
RX	MEDLINE=94032282; PubMed=7692964;
RA	Sherman P.A., Laubach V.E., Reep B.R., Wood E.R.;
RT	"Purification and cDNA sequence of an inducible nitric oxide synthase
RT	from a human tumor cell line.";
RL	Biochemistry 32:11600-11605(1993).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Chondrocytes;
RX	MEDLINE=94068614; PubMed=7504305;
RA	Charles I.G., Palmer R.M.J., Hickery M.S., Bayliss M.T.,
RA	Chubb A.P., Hall V.S., Moss D.W., Moncada S.;
RT	"Cloning, characterization, and expression of a cDNA encoding an
RT	inducible nitric oxide synthase from the human chondrocyte.";
RL	Proc. Natl. Acad. Sci. U.S.A. 90:11419-11423(1993).
RN	[4]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Articular chondrocytes;
RX	MEDLINE=94368816; PubMed=7522054;
RA	Maier R., Bibe G., Rediske J., Lotz M.;
RT	"Inducible nitric oxide synthase from human articular chondrocytes:
RT	cDNA cloning and analysis of mRNA expression.";
RL	Biochim. Biophys. Acta 1208:145-150(1994).
RN	[5]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Retina;
RX	MEDLINE=95091827; PubMed=7528017;
RA	Park C.S., Pardhasaradhi K., Gianotti C., Villegas E., Krishna G.;
RT	"Human retina expresses both constitutive and inducible isoforms of
RT	nitric oxide synthase mRNA.";

RL Biochem. Biophys. Res. Commun. 205:85-91(1994).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Glioblastoma;  
 RX MEDLINE=95155267; PubMed=7531687;  
 RA Hokari A., Zeniya M., Esumi H.;  
 RT "Cloning and functional expression of human inducible nitric oxide  
 synthase (NOS) cDNA from a glioblastoma cell line A-172.";  
 RL J. Biochem. 116:575-581(1994).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Airway epithelium;  
 RX MEDLINE=9537368; PubMed=7544004;  
 RA Guo F.H., de Raevae R.H., Rice T.W., Stuehr D.J., Thunnissen F.B.J.M.,  
 RA Erzurum S.C.;  
 RT "Continuous nitric oxide synthesis by inducible nitric oxide synthase  
 in normal human airway epithelium in vivo.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7809-7813(1995).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cardiac myocytes;  
 RX MEDLINE=97304504; PubMed=9160867;  
 RA Luss H., Li R.-K., Shapiro R.A., Tzeng E., McGowan F.X., Yoneyama T.,  
 RA Hatakeyama K., Geller D.A., Mickie D.A.G., Simmons R.L.,  
 RA Billiar T.R.;  
 RT "Differentiated human ventricular cardiac myocytes express  
 inducible nitric oxide synthase mRNA but not protein in response to  
 IL-1, TNF, IFN-gamma, and LPS.";  
 RL J. Mol. Cell. Cardiol. 29:1153-1165(1997).  
 RN [9]  
 RP SEQUENCE OF 380-473 FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=9516725; PubMed=7532248;  
 RA McJury J.S., Chatterjee P., Nicolson A.G., Jardine A.G., McKay N.G.,  
 RA Ralston S.H., Grabowski P., Haites N.E., Macleod A.M.,  
 RA Hawksworth G.M.;  
 RT "Nitric oxide production by human proximal tubular cells: a novel  
 immunomodulatory mechanism?";  
 RL Kidney Int. 46:1043-1049(1994).  
 RN [10]  
 RP CHARACTERIZATION.  
 RX MEDLINE=96047340; PubMed=7558036;  
 RA Bloch K.D., Wolflap J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G.,  
 RA Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;  
 RT "Three members of the nitric oxide synthase II gene family (NOS2A,  
 NOS2B, and NOS2C) colocalize to human chromosome 17.";  
 RL Genomics 27:526-530(1995).  
 RN [11]  
 RP CHARACTERIZATION.  
 RX MEDLINE=98389865; PubMed=9721329;  
 RA Taylor B.S., Alarcon L.H., Billiar T.R.;  
 RT "Inducible nitric oxide synthase in the liver: regulation and  
 function.";  
 RL Biochimica 63:766-781(1998).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 74-504.  
 RX MEDLINE=99340067; PubMed=10409685;  
 RA Li H., Raman C.S., Glaser C.B., Blasko E., Young T.A., Parkinson J.F.,  
 RA Whitlow M., Poulos T.L.;  
 RT "Crystal structures of zinc-free and -bound heme domain of human  
 inducible nitric-oxide synthase. Implications for dimer stability and  
 comparison with endothelial nitric-oxide synthase.";  
 RL J. Biol. Chem. 274:21276-21284(1999).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 82-528.  
 RX MEDLINE=99173237; PubMed=10074942;  
 RA Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,  
 RA Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,  
 RA Weber P.C.;  
 RT "Structural characterization of nitric oxide synthase isoforms  
 reveals striking active-site conservation.";  
 RL Nat. Struct. Biol. 6:233-242(1999).  
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE

CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO  
 CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.  
 CC -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) - CITRULLINE +  
 CC NITRIC OXIDE + N NADP(+).  
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 CC TETRAHYDROBIPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 CC THE ENZYME (BY SIMILARITY).  
 CC -1- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST  
 CC WITH MOUSE NOS2). ASPARIN INHIBITS EXPRESSION AND FUNCTION OF THIS  
 CC ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF  
 CC TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE  
 CC CATALYTIC ACTIVITY (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE LIVER, RETINA, BONE CELLS AND  
 CC AIRWAY EPITHELIAL CELLS OF THE LUNG. NOT EXPRESSED IN THE  
 CC PLATELETS.  
 CC -1- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES.  
 CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; L09210; AAA59171.1; -;  
 CC EMBL; L24553; AAA36375.1; -;  
 CC EMBL; X73029; CAA51512.1; -;  
 CC EMBL; U05810; AAA56666.1; -;  
 CC EMBL; U31511; AAB49041.1; -;  
 CC EMBL; D26525; BAA05531.1; -;  
 CC EMBL; U20141; AAB60366.1; -;  
 CC EMBL; AF068236; AAC19133.1; -;  
 CC EMBL; S75615; AAD14179.1; -;  
 CC PIR; A47475; A47475.  
 CC PDB; 1NSI; 07-JAN-00.  
 CC PDB; 2NSI; 07-JAN-00.  
 CC PDB; 4NOS; 04-FEB-00.  
 CC MIN; 163730; -;  
 CC InterPro; IPR001094; -;  
 CC InterPro; IPR001433; -;  
 CC InterPro; IPR001709; -;  
 CC InterPro; IPR003097; -;  
 CC Pfam; PF00667; FAD\_binding; 1.  
 CC Pfam; PF00175; oxidoreductase; 1.  
 CC PRINTS; PR00369; FLAVODOXIN.  
 CC PRINTS; PR00371; FPNCR.  
 CC Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;  
 CC Heme; Phosphorylation; Zinc; Metal-binding; Multigene family;  
 CC 3D-structure.  
 CC BINDING 200 200 HEME.  
 CC DOMAIN 509 529 CALMODULIN-BINDING (POTENTIAL).  
 CC NP\_BIND 623 654 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 CC NP\_BIND 767 778 FAD (ADP PART) (BY SIMILARITY).  
 CC NP\_BIND 903 913 FAD (FLAVIN PART) (BY SIMILARITY).  
 CC NP\_BIND 978 996 NADP (RIBOSE PART) (BY SIMILARITY).  
 CC NP\_BIND 1076 1091 NADP (ADP PART) (BY SIMILARITY).  
 CC METAL 110 110 ZINC.  
 CC METAL 115 115 ZINC.  
 CC MOD\_RES 234 234 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 CC MOD\_RES 578 578 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 CC MOD\_RES 892 892 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 CC CONFLICT 23 23 D -> G (IN REF. 4).  
 CC CONFLICT 154 154 F -> L (IN REF. 4).  
 CC CONFLICT 177 177 R -> V (IN REF. 4).  
 CC CONFLICT 266 266 R -> H (IN REF. 8).  
 CC CONFLICT 423 423 L -> I (IN REF. 2).  
 CC CONFLICT 439 439 A -> T (IN REF. 8).  
 CC CONFLICT 608 608 S -> L (IN REF. 5 AND 6).  
 CC CONFLICT 676 676 T -> I (IN REF. 7).  
 CC CONFLICT 800 800 T -> A (IN REF. 4).



Query Match 100.0%; Score 95; DB 1; Length 1153;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVQIGILRVVDGPTPH 18  
 |||||  
 Db 781 PALVQIGILRVVDGPTPH 798

RESULT 2  
 NOS2\_MOUSE  
 ID NOS2\_MOUSE STANDARD; PRT; 1144 AA.  
 AC P29477; O70515; O70516;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)  
 DE (INDUCIBLE NOS) (INOS) (MACROPHAGE NOS) (MAC-NOS).  
 GN NOS2 OR INOSL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92229444; PubMed=1373522;  
 RA Xie Q.-W., Cho H.-J., Calaycay J., Mumford R.A., Swiderek K.M.,  
 RA Lee T.D., Ding A., Troso T., Nathan C.;  
 RT "Cloning and characterization of inducible nitric oxide synthase from  
 RT mouse macrophages";  
 RL Science 256:225-228(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92357701; PubMed=1379716;  
 RA Lowenstein C.J., Glatt C.S., Bredt D.S., Snyder S.H.;  
 RT "Cloned and expressed macrophage nitric oxide synthase contrasts with  
 RT the brain enzyme";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92210618; PubMed=1372907;  
 RA Lyons C.R., Orloff G.J., Cunningham J.M.;  
 RT "Molecular cloning and functional expression of an inducible nitric  
 RT oxide synthase from a murine macrophage cell line";  
 RL J. Biol. Chem. 267:6370-6374(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96088781; PubMed=7503239;  
 RA Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.;  
 RT "Role of NF-kappa B in the regulation of inducible nitric oxide  
 RT synthase in an MTAL cell line";  
 RL Am. J. Physiol. 269:F718-F729(1995).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=DBA/2J, BALB/CBYJ, SJL/J, NOD/LTJ, AND B10.S/J; TISSUE=Spleen;  
 RA Ma R.Z., Teuscher C.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.  
 RX MEDLINE=97477482; PubMed=9334294;  
 RA Crane B.R., Arvai A.S., Gachhui R., Wu C., Ghosh D.K., Getzoff E.D.,  
 RA Stuehr D.J., Tainer J.A.;  
 RT "The structure of nitric oxide synthase oxygenase domain and  
 RT inhibitor complexes";  
 RL Science 278:425-431(1997).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.  
 RX MEDLINE=20031637; PubMed=10562538;  
 RA Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C.,  
 RA Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.;  
 RT "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin  
 RT hook and pterin-binding segment in dimerization and

tetrahydrobiopterin interaction.";

RL EMBO J. 18:6260-6270(1999).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.  
 RX MEDLINE=98182450; PubMed=9516116;  
 RA Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,  
 RA Tainer J.A.;  
 RT "Structure of nitric oxide synthase oxygenase dimer with pterin and  
 RT substrate";  
 RL Science 279:2121-2126(1998).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.  
 RX MEDLINE=20031638; PubMed=10562539;  
 RA Crane B.R., Rosenfeld R.J., Arvai A.S., Ghosh D.K., Ghosh S.,  
 RA Tainer J.A., Stuehr D.J., Getzoff E.D.;  
 RT "N-terminal domain swapping and metal ion binding in nitric oxide  
 RT synthase dimerization";  
 RL EMBO J. 18:6271-6281(1999).  
 RN [10]  
 RP EFFECT OF ASPIRIN.  
 RC TISSUE=Macrophage;  
 RX MEDLINE=95372392; PubMed=7544010;  
 RA Amin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,  
 RA Weissmann G., Abramson S.B.;  
 RT "The mode of action of aspirin-like drugs: effect on inducible nitric  
 RT oxide synthase";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).  
 CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO  
 CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.  
 CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +  
 CC NITRIC OXIDE + N NADP(+).  
 CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 CC TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 CC THE ENZYME.  
 CC -!- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN  
 CC INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE  
 CC EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL  
 CC MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY.  
 CC -!- SUBUNIT: HOMODIMER.  
 CC -!- TISSUE SPECIFICITY: MACROPHAGES.  
 CC -!- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES.  
 CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M87039; AAA39315.1; -;  
 DR EMBL; M92649; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; M84373; AAA39834.1; -;  
 DR EMBL; U43428; AAC52356.1; -;  
 DR EMBL; AF065919; AAC17914.1; -;  
 DR EMBL; AF065920; AAC17915.1; -;  
 DR EMBL; AF065921; AAC17916.2; -;  
 DR EMBL; AF065922; AAC17917.1; ALT\_INIT.  
 DR EMBL; AF065923; AAC17918.2; -;  
 DR PIR; A43271; A43271.  
 DR PIR; A42166; A42166.  
 DR PDB; 1NOC; 18-NOV-98.  
 DR PDB; 1NOC; 18-NOV-98.  
 DR PDB; 2NOS; 18-NOV-98.  
 DR PDB; 1NOD; 23-MAR-99.  
 DR PDB; 2NOD; 23-MAR-99.  
 DR PDB; 3NOD; 23-MAR-99.  
 DR PDB; 1DF1; 08-DEC-99.  
 DR PDB; 1DWV; 04-FEB-00.  
 DR PDB; 1DWX; 06-FEB-00.  
 DR PDB; 1DWX; 06-FEB-00.

```

DR PDB: 1QOM; 15-DEC-99.
DR PDB: 1DD7; 29-MAR-00.
DR MGD: MGI-97361; NOS2.
DR InterPro: IPR001094; -.
DR InterPro: IPR001433; -.
DR InterPro: IPR001709; -.
DR InterPro: IPR003097; -.
DR Pfam: PF00175; oxidored_fad; 1.
DR Pfam: PF00667; FAD_binding; 1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
KW Zinc; Metal-binding; Multigene family; 3D-structure.
FT BINDING 194 194
FT DOMAIN 503 523
FT NP_BIND 617 648
FT NP_BIND 761 772
FT NP_BIND 897 907
FT NP_BIND 972 990
FT NP_BIND 1070 1085
FT METAL 104 104
FT METAL 109 109
FT VARIANT 211 211
FT VARIANT 967 967
FT VARIANT 968 968
FT CONFLICT 19 19
FT CONFLICT 191 191
FT CONFLICT 844 844
SQ SEQUENCE 1144 AA; 130574 MW; 0735BE676113457F CRC64;

Query Match 83.2%; Score 79; DB 1; Length 1144;
Best Local Similarity 94.1%; Pred. No. 3.3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ALVQGILERVVDGTPPH 18
Db 776 ALVQGILERVVDCTPPH 792

RESULT 3
NOS2_CAVPO STANDARD; PRT; 1149 AA.
AC 054705;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
DE (INDUCIBLE NOS) (INOS).
GN NOS2 OR NOS.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARTLEY; TISSUE=Lung;
RX MEDLINE=98343971; PubMed=9677342;
RA Shirato M., Sakamoto T., Uchida Y., Nomura A., Ishii Y., Iijima H.,
RA Goto Y., Hasegawa S.;
RT "Molecular cloning and characterization of Ca2+-dependent inducible
RL nitric oxide synthase from guinea-pig lung.";
RL Biochem. J. 333:795-799(1998).
CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.
CC -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) -> CITRULLINE +
CC NITRIC OXIDE + N NADP(+).
CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME (BY SIMILARITY).
CC -1- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST
CC WITH MOUSE NOS2).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

```

```

CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE LUNG AND COLON. NOT DETECTED
CC IN THE HEART, AORTA, LIVER, KIDNEY, AND SPLEEN.
CC -1- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS) IN KIDNEY, SPLEEN, AND
CC COLON. EXPRESSION IS REDUCED IN THE PRESENCE OF LPS IN LUNG.
CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.
-----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL: AF027180; AAC33177.1; -.
CC HSP: P29477; 2NOS.
CC InterPro: IPR001094; -.
CC InterPro: IPR001433; -.
CC InterPro: IPR001709; -.
CC InterPro: IPR003097; -.
CC Pfam: PF00667; FAD_binding; 1.
CC Pfam: PF00175; oxidored_fad; 1.
CC PRINTS: PR00369; FLAVODOXIN.
CC PRINTS: PR00371; FPNCR.
KW Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;
KW Heme; Multigene family.
FT BINDING 199 199
FT DOMAIN 508 528
FT NP_BIND 622 653
FT NP_BIND 766 777
FT NP_BIND 902 912
FT NP_BIND 977 995
FT NP_BIND 1075 1090
SQ SEQUENCE 1149 AA; 130631 MW; 66D595A2486DB50E CRC64;

Query Match 77.9%; Score 74; DB 1; Length 1149;
Best Local Similarity 83.3%; Pred. No. 0.00022;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PALVQGILERVVDGTPPH 18
Db 780 PALVQGILECVVDNPGPH 797

RESULT 4
NOS2_RAT STANDARD; PRT; 1147 AA.
AC 006518; P97774; Q35765; Q35766; Q64558; Q64005; Q63267;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
DE (INDUCIBLE NOS) (INOS).
GN NOS2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vascular smooth muscle;
RX MEDLINE=93191721; PubMed=7680561;
RA Nunokawa Y., Ishida N., Tanaka S.;
RT "Cloning of inducible nitric oxide synthase in rat vascular smooth
RL muscle cells.";
RL Biochem. Biophys. Res. Commun. 191:89-94(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=Pancreatic islets;
RX MEDLINE=95309542; PubMed=7540573;
RA Karlens A.E., Andersen H.O., Vissing H., Larsen P.M., Fey S.J.,
RA Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,

```

RA Mandrup-Poulsen T., Boel E., Nerup J.;  
 RT "Cloning and expression of cytokine-inducible nitric oxide synthase  
 RT cDNA from rat islets of Langerhans.";  
 RL Diabetes 44:753-758(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Astocytes;  
 RX MEDLINE=94231594; PubMed=7513765;  
 RA Galea E., Reis D.J., Feinstein D.L.;  
 RT "Cloning and expression of inducible nitric oxide synthase from rat  
 RT astrocytes.";  
 RL J. Neurosci. Res. 37:406-414(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=94039059; PubMed=7693462;  
 RA Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K.,  
 RT "Molecular cloning of a cDNA encoding an inducible  
 RT calmodulin-dependent nitric-oxide synthase from rat liver and its  
 RT expression in COS 1 cells.";  
 RL Eur. J. Biochem. 217:37-43(1993).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Hepatocytes;  
 RX MEDLINE=93221515; PubMed=7682072;  
 RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;  
 RT "Hepatocytes and macrophages express an identical cytokine inducible  
 RT nitric oxide synthase gene.";  
 RL Biochem. Biophys. Res. Commun. 191:767-774(1993).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Aorta;  
 RX MEDLINE=94325351; PubMed=7519448;  
 RA Geng Y.J., Almqvist M., Hansson G.K.;  
 RT "cDNA cloning and expression of inducible nitric oxide synthase from  
 RT rat vascular smooth muscle cells.";  
 RL Biochim. Biophys. Acta 1218:421-424(1994).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC Kousuga K., Yui Y., Hattori R., Sase K., Ezawa H., Aoyama T.,  
 RA Inoue R., Sasayama S.;  
 RT "Cloning of an inducible nitric oxide synthase from rat  
 RT polymorphonuclear neutrophils.";  
 RL Endothelium 2:217-221(1994).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97070590; PubMed=8913516;  
 RA Tsutsumishita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,  
 RA Putaki S., Niwa M.;  
 RT "Sequence analysis of inducible nitric oxide synthase in rat kidney,  
 RT lung, and uterus.";  
 RL Biol. Pharm. Bull. 19:1374-1376(1996).  
 RN [9]  
 RP SEQUENCE OF 426-788 FROM N.A.  
 RC STRAIN=DAHL/RAPP SALT SENSITIVE STRAIN; TISSUE=Vascular smooth muscle;  
 RX MEDLINE=98195092; PubMed=9535415;  
 RA Chen P.Y., Gladish R.D., Sanders P.W.;  
 RT "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp  
 RT salt-sensitive rats.";  
 RL Hypertension 31:918-924(1998).  
 RN [10]  
 RP SEQUENCE OF 509-740 FROM N.A.  
 RC STRAIN=WISTAR; TISSUE=Renal glomerulus;  
 RA Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;  
 RT "Advances in the studies of NO synthesis regulation in mesangial  
 RT cells.";  
 RL Neurologia 16:35-39(1996).  
 RN [11]  
 RP SEQUENCE OF 479-655 FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Renal glomerulus;  
 RX MEDLINE=94276509; PubMed=7516453;  
 RA Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montani D.,

RA Klahr S.;  
 RT "Location of an inducible nitric oxide synthase mRNA in the normal  
 RT kidney.";  
 RL Kidney Int. 45:998-1005(1994).  
 RN [12]  
 RP SEQUENCE OF 420-479 FROM N.A.  
 RC TISSUE=Myocardium;  
 RX Michel T., Balligand J.-L.;  
 RT "Isolation and characterization of iNOS from rat cardiocytes.";  
 RL Subst. (SEP-1994) to the EMBL/GenBank/DBJ databases.  
 CC -I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.  
 CC -I- CATALYTIC ACTIVITY: L-ARGININE + NADPH + M O(2) - CITRULLINE +  
 CC NITRIC OXIDE + N NADP(+).  
 CC -I- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 CC THE ENZYME.  
 CC -I- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN  
 CC INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE  
 CC EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL  
 CC MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY  
 CC SIMILARITY).  
 CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -I- TISSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY IN THE  
 CC MEDULLARY THICK ASCENDING LIMB, WITH MINOR AMOUNTS IN THE  
 CC MEDULLARY COLLECTING DUCT AND VASA RECTA BUNDLE.  
 CC -I- INDUCTION: BY INTERFERON GAMMA AND LIPOPOLYSACCHARIDE.  
 CC -I- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL: D14051; BAA03138.1; -;  
 DR EMBL: U26686; AAB5861.1; -;  
 DR EMBL: U03699; AAC13747.1; -;  
 DR EMBL: D12520; BAA02090.1; -;  
 DR EMBL: L12562; AAA1720.1; -;  
 DR EMBL: X76881; CAA54208.1; -;  
 DR EMBL: D4591; BAA07994.1; -;  
 DR EMBL: D83661; BAA12035.1; -;  
 DR EMBL: AF006619; AAC16401.1; -;  
 DR EMBL: U48829; AAB18620.1; -;  
 DR EMBL: S71597; AAB31028.2; -;  
 DR EMBL: L36063; AAC02242.1; -;  
 DR PIR: JC1472; JC1472.  
 DR HSSP: P29477; INOC.  
 DR InterPro: IPR001094; -;  
 DR InterPro: IPR001433; -;  
 DR InterPro: IPR001709; -;  
 DR InterPro: IPR003097; -;  
 DR Pfam: PF00667; FAD\_binding; 1.  
 DR Pfam: PF00175; oxidored\_fad; 1.  
 DR PRINTS: PR00369; FLAVODOXIN.  
 DR PRINTS: PR00371; FPNCR.  
 KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;  
 KW Zinc; Metal-binding; Multigene family.  
 FT BINDING 197 197  
 FT DOMAIN 506 526  
 FT NP\_BIND 620 651  
 FT NP\_BIND 764 775  
 FT NP\_BIND 900 910  
 FT NP\_BIND 975 993  
 FT NP\_BIND 1073 1088  
 FT METAL 107 107  
 FT METAL 112 112  
 FT CONFLICT 10 10  
 FT CONFLICT 72 72  
 H -> Y (IN REF. 1).

```

FT CONFLICT 107 C -> R (IN REF. 3).
FT CONFLICT 128 D -> V (IN REF. 8).
FT CONFLICT 130 P -> H (IN REF. 3).
FT CONFLICT 171 E -> G (IN REF. 8).
FT CONFLICT 195 P -> S (IN REF. 8).
FT CONFLICT 248 S -> T (IN REF. 3 AND 5).
FT CONFLICT 264 Y -> I (IN REF. 3).
FT CONFLICT 277 D -> E (IN REF. 3).
FT CONFLICT 348 A -> P (IN REF. 1).
FT CONFLICT 349 V -> A (IN REF. 6).
FT CONFLICT 380 F -> L (IN REF. 2, 7 AND 8).
FT CONFLICT 395 R -> S (IN REF. 4).
FT CONFLICT 412 V -> A (IN REF. 3).
FT CONFLICT 477 M -> I (IN REF. 12).
FT CONFLICT 513 L -> W (IN REF. 11).
FT CONFLICT 515 L -> W (IN REF. 11).
FT CONFLICT 545 G -> R (IN REF. 11).
FT CONFLICT 551 A -> R (IN REF. 10).
FT CONFLICT 556 A -> S (IN REF. 11).
FT CONFLICT 564 T -> N (IN REF. 11).
FT CONFLICT 570 E -> D (IN REF. 11).
FT CONFLICT 583 L -> P (IN REF. 5 AND 9).
FT CONFLICT 591 G -> A (IN REF. 11).
FT CONFLICT 591 G -> V (IN REF. 1 AND 6).
FT CONFLICT 619 A -> R (IN REF. 2).
FT CONFLICT 664 D -> G (IN REF. 10).
FT CONFLICT 679 ET -> VP (IN REF. 1).
FT CONFLICT 690 Q -> P (IN REF. 10).

Query Match 62.1%; Score 59; DB 1; Length 1147;
Best Local Similarity 81.2%; Pred. No. 0.071;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALVQGLERVDGPTP 17
DB 779 ALVQGLERVDGPTP 794

RESULT 5
NS2D_HUMAN STANDARD; PRT; 1147 AA.
AC O60591; O60604;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE NITRIC OXIDE SYNTHASE, INDUCIBLE IID (EC 1.14.13.39) (NOS, TYPE II D)
DE (INDUCIBLE NOS) (INOS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle, and Heart muscle;
RX MEDLINE=99066690; PubMed=9851365;
RA Adams V., Krabbes S., Jiang H., Yu J., Rahmel A., Gielen S.,
RA Schuler G., Hambrecht R.;
RT "Complete coding sequence of inducible nitric oxide synthase from
RT human heart and skeletal muscle of patients with chronic heart
RT failure.";
RL Nitric oxide 2:242-249(1998).
CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO
CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS. MAY BE INVOLVED IN
CC THE PATHOGENESIS OF DILATED CARDIOMYOPATHY OR OF EXERCISE
CC INTOLERANCE OBSERVED IN PATIENTS WITH CHRONIC HEART FAILURE.
CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) -> CITRULLINE +
CC NITRIC OXIDE + N NADP(+).
CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME (BY SIMILARITY).
CC -!- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (BY
CC SIMILARITY).

```

-!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 -!- TISSUE SPECIFICITY: EXPRESSED IN THE HEART AND SKELETAL MUSCLE DURING CHRONIC HEART FAILURE, BUT NOT IN HEALTHY INDIVIDUALS.  
 -!- SIMILARITY: BELONGS TO THE NOS FAMILY.

-----  
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----

EMBL; AF049656; AAC83553.1; -;  
 EMBL; AF051164; AAC83554.1; -;  
 HSSP; P29477; INOC.  
 InterPro; IPR001094; -;  
 InterPro; IPR001433; -;  
 InterPro; IPR001709; -;  
 InterPro; IPR003097; -;  
 Pfam; PF00667; FAD\_binding; 1.  
 Pfam; PF00175; Oxidoreductase; 1.  
 PRINTS; PR00369; FLAVODOXIN.  
 PRINTS; PR00371; FPNCR.  
 KW Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;  
 KW Heme; Zinc; Metal-binding; Multigene family;  
 FT BINDING 197 197  
 FT DOMAIN 506 526  
 FT NP\_BIND 620 651  
 FT NP\_BIND 764 775  
 FT NP\_BIND 900 910  
 FT NP\_BIND 975 993  
 FT NP\_BIND 1073 1088  
 FT METAL 107 107  
 FT METAL 112 112  
 FT CONFLICT 248 248  
 FT CONFLICT 271 271  
 FT CONFLICT 399 399  
 FT CONFLICT 640 640  
 FT CONFLICT 731 731  
 FT CONFLICT 937 937  
 FT CONFLICT 1008 1009  
 FT CONFLICT 1024 1024  
 FT CONFLICT 1076 1076  
 FT CONFLICT 1129 1129  
 FT CONFLICT 1147 1147  
 SQ SEQUENCE 1147 AA; 130528 MW; FF7E4C7ABA76D820 CRC64;

Query Match 62.1%; Score 59; DB 1; Length 1147;  
 Best Local Similarity 81.2%; Pred. No. 0.071;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALVQGLERVDGPTP 17  
 DB 779 ALVQGLERVDGPTP 794

RESULT 6  
 NOS2\_RABIT STANDARD; PRT; 496 AA.  
 ID NOS2\_RABIT  
 AC O19114;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)  
 DE (INDUCIBLE NOS) (INOS) (FRAGMENT).  
 OS Oryctolagus cuniculus (Rabbit).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.

```

Query Match      57.9%; Score 55; DB 1; Length 496;
Best Local Similarity 80.0%; Pred. No. 0.13;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3  LVQILERVVDGPTP 17
          ||| ||||| |
Db      154  LVQILERVVDCSSP 168

```

```

RESULT      7
YHCR_BACSU
ID  YHCR_BACSU      STANDARD;      PRT;  1217 AA.
AC  P54602;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  30-MAY-2000 (Rel. 39, Last annotation update)
DE  DE HYPOTHETICAL 132.7 KDA PROTEIN IN CSPB-GLPP INTERGENIC REGION.
GN  YHCR.
OS  Bacillus subtilis.
OC  Bacteria: Firmicutes; Bacillus/Clostridium group;
OC  Bacillus/Staphylococcus group; Bacillus.
OX  NCBI_TaxId=1423;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=168;
RX  MEDLINE=97124185; PubMed=8969498;
RA  Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S.;
RT  'A 22 kb DNA sequence in the csbB-glppFKD region at 75 degrees on the
RT  Bacillus subtilis chromosome.';
RL  Microbiology 142:3021-3026(1996).
CC  -!- SIMILARITY: IN THE C-TERMINAL SECTION: BELONGS TO THE 5'-

```

```

CC CC NUCLEOTIDASE FAMILY.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: X96983; CAA65702.1; -
CC CC EMBL: Z99108; CAB12747.1; -
CC CC HSSP: P00644; ZSOB.
CC CC Subtilist; BGLI596; YhcR.
CC CC InterPro: IPR000080; -
CC CC InterPro: IPR001899; -
CC CC InterPro: IPR002224; -
CC CC Pfam: PF01009; 5_nucleotidase; 1.
CC CC Pfam: PF00746; Gram_pos_anchor; 1.
CC CC Pfam: PF00565; Snaase; 1.
CC CC PROSITE; PS00785; 5_NUCLEOTIDASE_1; FALSE_NEG.
CC CC PROSITE; PS00786; 5_NUCLEOTIDASE_2; 1.
CC CC KW Hypothetical protein; Hydrolase.
CC CC SEQUENCE 1217 AA; 132586 MW; 7973160CC898DC0B CRC64;
CC -----
CC CC
CC CC Query Match 51.6%; Score 49; DB 1; Length 1217;
CC CC Best Local Similarity 64.3%; Pred. No. 3.6;
CC CC Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC CC
CC CC QY 5 OGILERVVDGPTPH 18
CC CC :||:|||||
CC CC Db 379 EGVDRVVDGDTIH 392
CC CC
CC CC RESULT 8
CC CC NOS3_HUMAN
CC CC ID NOS3_HUMAN STANDARD; PRT; 1202 AA.
CC CC P29474; Q14251; Q14434; Q13662;
CC CC 01-APR-1993 (Rel. 25, Created)
CC CC DT 01-JUL-1993 (Rel. 26, Last sequence update)
CC CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC CC DE NITRIC-OXIDE SYNTHASE, ENDOTHELIAL (EC 1.14.13.39) (EC-NOS) (NOS, TYPE
CC CC III) (NOSIII) (ENDOTHELIAL NOS) (ENOS) (CONSTITUTIVE NOS) (CNOS).
CC CC NOS3.
CC CC OS Homo sapiens (Human).
CC CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC CC NCBI_TaxID=9606;
CC CC [1]
CC CC RP SEQUENCE FROM N.A.
CC CC RX MEDLINE=92340475; PubMed=1378832;
CC CC RA Janssens S.P., Shimouchi A., Quertermous T., Bloch D.B., Bloch K.D.;
CC CC RT "Cloning and expression of a cDNA encoding human endothelium-derived
CC CC RT relaxing factor/nitric oxide synthase.";
CC CC J. Biol. Chem. 267:14519-14522(1992).
CC CC [2]
CC CC RN ERRATUM.
CC CC RA Janssens S.P., Shimouchi A., Quertermous T., Bloch D.B., Bloch K.D.;
CC CC RL J. Biol. Chem. 267:22694-22694(1992).
CC CC [3]
CC CC RN SEQUENCE FROM N.A.
CC CC RP MEDLINE=92354731; PubMed=1379542;
CC CC RA Marsden P.A., Schappert K.T., Chen H.S., Flowers M., Sundell C.L.,
CC CC RL Wilcox J.N., Lamas S., Michel T.;
CC CC RT "Molecular cloning and characterization of human endothelial nitric
CC CC RT oxide synthase.";
CC CC FEBS Lett. 307:287-293(1992).
CC CC [4]
CC CC RN SEQUENCE FROM N.A.
CC CC RP MEDLINE=93352539; PubMed=7688726;
CC CC RA Marsden P.A., Heng H.H., Scherer S.W., Stewart R.J., Hall A.V.,
CC CC RA Shi X.M., Tsui L.C., Schappert K.T.;

```

RT "Structure and chromosomal localization of the human constitutive  
RT endothelial nitric oxide synthase gene.";  
RL J. Biol. Chem. 268:17478-17488(1993).  
RN [5]  
RC SEQUENCE FROM N.A.  
RP TISSUE:Umbilical vein;  
RA Liao J.K.;  
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE:Placenta;  
RX MEDLINE-94161710; PubMed-7509596;  
RA Nadaud S.A., Bonnardeux A., Lathrop M., Soubrier F.;  
RT "Gene structure, polymorphism and mapping of the human endothelial  
RT nitric oxide synthase gene.";  
RL Biochem. Biophys. Res. Commun. 198:1027-1033(1994).  
RN [7]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-94333373; PubMed-7519887;  
RA Miyahara K., Kawamoto T., Sase K., Yui Y., Toda K., Yang L.X.,  
RA Hattori R., Aoyama T., Yamamoto Y., Doi Y., Ogoshi S.,  
RA Hashimoto K., Kawai C., Sasayama S., Shizuta Y.;  
RT "Cloning and structural characterization of the human endothelial  
RT nitric-oxide-synthase gene.";  
RL Eur. J. Biochem. 223:719-726(1994).  
RN [8]  
RP SEQUENCE OF 1-52 FROM N.A.  
RC TISSUE:Placenta;  
RX MEDLINE-94245207; PubMed-7514568;  
RA Robinson L.J., Węremowicz S., Morton C.C., Michel T.;  
RT "Isolation and chromosomal localization of the human endothelial  
RT nitric oxide synthase (NOS3) gene.";  
RL Genomics 19:350-357(1994).  
RN [9]  
RP SEQUENCE OF 410-527 FROM N.A.  
RC TISSUE:Platelet;  
RX MEDLINE-96077182; PubMed-7475956;  
RA Sase K., Michel T.;  
RT "Expression of constitutive endothelial nitric oxide synthase in human  
RT blood platelets.";  
RL Life Sci. 57:2049-2055(1995).  
RN [10]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
RX MEDLINE-99173237; PubMed-10074942;  
RA Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,  
RA Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,  
RA Weber P.C.;  
RT "Structural characterization of nitric oxide synthase isoforms  
RT reveals striking active-site conservation.";  
RL Nat. Struct. Biol. 6:233-242(1999).  
RN [11]  
RP VARIANT CORONARY SPASM ASP-297.  
RX MEDLINE-98407797; PubMed-9737779;  
RA Yoshimura M., Yasue H., Nakayama M., Shimasaki Y., Sumida H.,  
RA Sugiyama S., Kugiyama K., Ogawa H., Ogawa Y., Saito Y., Miyamoto Y.,  
RA Nakao K.;  
RT "A missense Glu298Asp variant in the endothelial nitric oxide synthase  
RT gene is associated with coronary spasm in the Japanese.";  
RL Hum. Genet. 103:65-69(1998).  
CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN  
CC VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A CGMP-MEDIATED SIGNAL  
CC TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH  
CC FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND  
CC PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS.  
CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) -> CITRULLINE +  
CC NITRIC OXIDE + N NADP(+).  
CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
CC THE ENZYME.  
CC -!- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN.  
CC -!- SUBUNIT: HOMODIMER.  
CC -!- TISSUE SPECIFICITY: PLATELETS.  
CC -!- DISEASE: DEFECTS IN NOS3 ARE INVOLVED IN CORONARY SPASM.

CC CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M93718; AAA36364.1; -;  
CC EMBL; M95296; AAA36372.1; -;  
CC EMBL; L10709; AAA36365.1; -;  
CC EMBL; L10693; AAA36365.1; JOINED.  
CC EMBL; L10694; AAA36365.1; JOINED.  
CC EMBL; L10695; AAA36365.1; JOINED.  
CC EMBL; L10696; AAA36365.1; JOINED.  
CC EMBL; L10697; AAA36365.1; JOINED.  
CC EMBL; L10698; AAA36365.1; JOINED.  
CC EMBL; L10699; AAA36365.1; JOINED.  
CC EMBL; L10700; AAA36365.1; JOINED.  
CC EMBL; L10701; AAA36365.1; JOINED.  
CC EMBL; L10702; AAA36365.1; JOINED.  
CC EMBL; L10703; AAA36365.1; JOINED.  
CC EMBL; L10704; AAA36365.1; JOINED.  
CC EMBL; L10705; AAA36365.1; JOINED.  
CC EMBL; L10706; AAA36365.1; JOINED.  
CC EMBL; L10707; AAA36365.1; JOINED.  
CC EMBL; L10708; AAA36365.1; JOINED.  
CC EMBL; L26914; AAA36374.1; -;  
CC EMBL; W76303; CAA53950.1; -;  
CC EMBL; W76304; CAA53950.1; JOINED.  
CC EMBL; W76305; CAA53950.1; JOINED.  
CC EMBL; W76306; CAA53950.1; JOINED.  
CC EMBL; W76307; CAA53950.1; JOINED.  
CC EMBL; W76308; CAA53950.1; JOINED.  
CC EMBL; W76309; CAA53950.1; JOINED.  
CC EMBL; W76310; CAA53950.1; JOINED.  
CC EMBL; W76311; CAA53950.1; JOINED.  
CC EMBL; W76312; CAA53950.1; JOINED.  
CC EMBL; W76313; CAA53950.1; JOINED.  
CC EMBL; W76314; CAA53950.1; JOINED.  
CC EMBL; W76315; CAA53950.1; JOINED.  
CC EMBL; W76316; CAA53950.1; JOINED.  
CC EMBL; D26607; BAA05652.1; -;  
CC EMBL; L23210; AAA36373.1; -;  
CC EMBL; S80791; AAD14336.1; -;  
CC PIR; S24052; S24052.  
CC PIR; A42867; A42867.  
CC PDB; 3NOS; 04-FEB-00.  
CC MIM; 163729; -;  
CC InterPro; IPR001094; -;  
CC InterPro; IPR001433; -;  
CC InterPro; IPR001709; -;  
CC InterPro; IPR003097; -;  
CC Pfam; PF00667; FAD\_binding; 1.  
CC Pfam; PF00175; oxidoreductase; 1.  
CC PRINTS; PR00369; FLAVODOXIN.  
CC PRINTS; PR00371; FPNCR.  
CC Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;  
CC Lipoprotein; Palmitate; Disease mutation; Calcium-binding; Heme;  
CC Zinc; Metal-binding; Multigene family; 3D-structure.  
CC INIT\_MET 0 0  
CC BINDING 183 183  
CC DOMAIN 490 509  
CC NP\_BIND 648 679  
CC NP\_BIND 732 803  
CC NP\_BIND 934 944  
CC NP\_BIND 1009 1027  
CC NP\_BIND 1107 1122  
CC LIPID 1 1  
CC LIPID 14 14  
CC LIPID 25 25  
CC HEME (BY SIMILARITY).  
CC CALMODULIN-BINDING (POTENTIAL).  
CC FMN (PYRIMIDINE PART) (BY SIMILARITY).  
CC FAD (ADP PART) (BY SIMILARITY).  
CC FAD (FLAVIN PART) (BY SIMILARITY).  
CC NADP (RIBOSE PART) (BY SIMILARITY).  
CC NADP (ADP PART) (BY SIMILARITY).  
CC MYRISTATE (BY SIMILARITY).  
CC PALMITATE (BY SIMILARITY).  
CC PALMITATE (BY SIMILARITY).







Query Match 48.4%; Score 46; DB 1; Length 2290;  
 Best Local Similarity 64.3%; Pred. No. 22;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 QGILRVVDGPTPH 18  
 || |||: ||| |  
 Db 1830 QGALERLPDGPRIH 1843

RESULT 12  
 POLG\_EMCVB STANDARD; PRT: 2292 AA.  
 AC PL1593;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS  
 DE P2A TO P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C  
 DE (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D  
 DE (EC 2.7.7.48)]  
 OS Encephalomyocarditis virus (strain emc-b nondiabetogenic).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 OC Cardiovirus.  
 OX NCBI\_TaxID=12105;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89243189; PubMed=2541543;  
 RA Bae Y.S., Eun H.M., Yoon J.W.;  
 RT "Genomic differences between the diabetogenic and nondiabetogenic  
 variants of encephalomyocarditis virus."  
 RL Virology 170:282-287(1989).  
 CC O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.  
 CC -!- FUNCTION: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS.  
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,  
 CC VP3, AND VP4.  
 CC -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,  
 CC VP3, AND VP4.  
 CC -!- PTM: SPECIFIC ENZYMOLOGICAL CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
 CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M22457; AAA43033.1; ALT\_SEQ.  
 DR PIR; B31473; GNNYEB.  
 DR HSSP; P12296; IMEC.  
 DR MEROPS; C03.009; -.  
 DR MEROPS; U29.001; -.  
 DR InterPro; IPR000605; -.  
 DR InterPro; IPR001205; -.  
 DR InterPro; IPR001676; -.  
 DR Pfam; PF00680; RNA\_dep\_RNA\_pol; 1.  
 DR Pfam; PF00910; RNA\_helicase; 1.  
 DR Pfam; PF00073; rhv; 3.  
 DR Polyprotein; Core protein; Core protein; Transferase;  
 KW RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate.  
 FT PROPEP 1 67  
 FT CHAIN 68 137  
 FT CHAIN 138 393  
 FT CHAIN 394 624  
 FT CHAIN 625 901  
 FT CHAIN 902 1058  
 FT CHAIN 1059 1194  
 FT CHAIN 1195 1519  
 FT CHAIN 1520 1607  
 FT CHAIN 1608 1627  
 FT CHAIN 1628 1832  
 FT CHAIN 1628 1832

FT CHAIN 1833 2292 RNA-DIRECTED RNA POLYMERASE P3D (E).  
 FT LIPID 68 MYRISTATE (BY SIMILARITY).  
 FT ACT\_SITE 1786 PROTEASE (POTENTIAL).  
 FT ACT\_SITE 1804 PROTEASE (POTENTIAL).  
 SQ SEQUENCE 2292 AA; 255495 MW; 8540D0EB1437E8D4 CRC64;

Query Match 48.4%; Score 46; DB 1; Length 2292;  
 Best Local Similarity 64.3%; Pred. No. 22;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 QGILRVVDGPTPH 18  
 || |||: ||| |  
 Db 1832 QGALERLPDGPRIH 1845

RESULT 13  
 POLG\_EMCVD STANDARD; PRT: 2292 AA.  
 AC PL1594;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS  
 DE P2A TO P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C  
 DE (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D  
 DE (EC 2.7.7.48)]  
 OS Encephalomyocarditis virus (strain emc-d diabetogenic).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 OC Cardiovirus.  
 OX NCBI\_TaxID=12106;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89243189; PubMed=2541543;  
 RA Bae Y.S., Eun H.M., Yoon J.W.;  
 RT "Genomic differences between the diabetogenic and nondiabetogenic  
 variants of encephalomyocarditis virus."  
 RL Virology 170:282-287(1989).  
 CC O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.  
 CC -!- FUNCTION: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS.  
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,  
 CC VP3, AND VP4.  
 CC -!- PTM: SPECIFIC ENZYMOLOGICAL CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
 CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M22458; AAA43034.1; -.  
 DR PIR; A31473; GNNYED.  
 DR HSSP; P12296; IMEC.  
 DR MEROPS; C03.009; -.  
 DR MEROPS; U29.001; -.  
 DR InterPro; IPR000605; -.  
 DR InterPro; IPR001205; -.  
 DR InterPro; IPR001676; -.  
 DR Pfam; PF00680; RNA\_dep\_RNA\_pol; 1.  
 DR Pfam; PF00910; RNA\_helicase; 1.  
 DR Pfam; PF00073; rhv; 3.  
 DR Polyprotein; Coa protein; Core protein; Transferase;  
 KW RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate.  
 FT PROPEP 1 67  
 FT CHAIN 68 137  
 FT CHAIN 138 393  
 FT CHAIN 394 624  
 FT CHAIN 625 901  
 FT CHAIN 902 1058  
 FT CHAIN 902 1058

FT CHAIN 1059 1194 CORE PROTEIN P2B (I).  
 FT CHAIN 1195 1519 CORE PROTEIN P2C (F).  
 FT CHAIN 1520 1607 CORE PROTEIN P3A.  
 FT CHAIN 1608 1627 GENOME-LINKED PROTEIN VPG (H).  
 FT CHAIN 1628 1832 PICORNAIN 3C (P22).  
 FT CHAIN 1833 2292 RNA-DIRECTED RNA POLYMERASE P3D (E).  
 FT LIPID 68 68 MYRISTATE (BY SIMILARITY).  
 FT ACT\_SITE 1786 1786 PROTEASE (POTENTIAL).  
 FT ACT\_SITE 1804 1804 PROTEASE (POTENTIAL).  
 SQ SEQUENCE 2292 AA; 255426 MW; F2B0627B0F444107 CRC64;

Query Match 48.4%; Score 46; DB 1; Length 2292;  
 Best Local Similarity 64.3%; Pred. No. 22;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 QGILRVVDGPPH 18  
 |||||  
 DB 1832 QGALERLPDGRH 1845

RESULT 14  
 MURB\_MYCTU  
 ID MURB\_MYCTU STANDARD; PRT; 369 AA.  
 AC Q11148;  
 DT 01-OCT-1996 (Rel. 34, Last Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE UDP-N-ACETYLENOLPYROVYLGLUCOSAMINE REDUCTASE (EC 1.1.1.158) (UDP-N-  
 ACETYLURAMATE DEHYDROXYLASE).  
 DE MURB OR RV0482 OR MTCY20G.08.  
 GN Mycobacterium tuberculosis.  
 OS Mycobacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Mycobacterium.  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch K., Parkhill J., Garnier T., Churcher C., Harris D.,  
 Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,  
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 Rutter S., Seeger K., Skellon S., Squares S., Squares K., Sulston J.E.,  
 Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 CC -|- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).  
 CC -|- CATALYTIC ACTIVITY: UDP-N-ACETYLURAMATE + NADP(+) ->  
 CC -|- UDP-N-ACETYL-3-O-(1-CARBOXYVINYL)-D-GLUCOSAMINE + NADPH.  
 CC -|- COFACTOR: FAD (BY SIMILARITY).  
 CC -|- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.  
 CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).  
 CC -|- SIMILARITY: BELONGS TO THE MURB FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; 277162; CAB00943.1; -;  
 DR HSSP; P08373; IMPT;  
 DR TubercuList; Rv0482; -;  
 KW Peptidoglycan synthesis; Cell wall; Cell division; Oxidoreductase;  
 KW NADP; Flavoprotein; FAD.  
 SQ SEQUENCE 369 AA; 38521 MW; 50AC021602ED9822 CRC64;

Query Match 47.9%; Score 45.5; DB 1; Length 369;  
 Best Local Similarity 36.0%; Pred. No. 3.8;  
 Matches 9; Conservative 3; Mismatches 6; Indels 7; Gaps 1;

QY 1 PALVQGILERVV-----DGTPPH 18  
 | : | : | :  
 DB 262 PVVTQDVVVERLAGDAATRKDGVPVH 286

RESULT 15  
 CLPB\_ECOLI  
 ID CLPB\_ECOLI STANDARD; PRT; 857 AA.  
 AC P03815;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE CLPB PROTEIN (HEAT SHOCK PROTEIN F84.1).  
 DE CLPB OR HTPM.  
 GN Escherichia coli.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90239044; PubMed=2185473;  
 RA Gottesman S., Squires C., Pichersky E., Carrington M., Hobbs M.,  
 Mattick J.S., Dairymple B., Kuramitsu H., Shiroza T., Foster T.,  
 Clark W.P., Ross B., Squires C.L., Maurizi M.R.;  
 RT "Conservation of the regulatory subunit for the Clp ATP-dependent  
 RT protease in prokaryotes and eukaryotes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3513-3517(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RA Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,  
 Ikenoto K., Inada T., Isono K., Itoh T., Kanai K., Kasai H.,  
 Kashimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K.,  
 Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y.,  
 Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,  
 Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-593 FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=91294165; PubMed=1906060;  
 RA Kitagawa M., Wada C., Yoshioaka S., Yura T.;  
 RT "Expression of ClpB, an analog of the ATP-dependent protease  
 RT regulatory subunit in Escherichia coli, is controlled by a heat shock  
 RT sigma factor (sigma 32).";  
 RL J. Bacteriol. 173:4247-4253(1991).  
 RN [5]  
 RP SEQUENCE OF 753-857 FROM N.A.  
 RX MEDLINE=82247208; PubMed=6285294;  
 RA Shen W.-F., Squires C., Squires C.L.;  
 RT "Nucleotide sequence of the rrmG ribosomal RNA promoter region of  
 RT Escherichia coli.";  
 RL Nucleic Acids Res. 10:3303-3313(1982).  
 RN [6]  
 RP SEQUENCE OF 1-31 FROM N.A.  
 RC STRAIN=K12 / W3110;  
 RA Ogura T., Tomoyasu T.;  
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.

Search completed: September 10, 2001, 14:09:53  
Job time: 562 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:01:14 ; Search time 42.28 Seconds  
(without alignments)  
32.430 Million cell updates/sec

Title: US-08-833-506C-30

Perfect score: 95  
Sequence: 1 PALVQGLERWVDGPTPH 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	95	100.0	1153	2 A49676	nitric-oxide synth
2	79	83.2	1144	1 A43271	nitric-oxide synth
3	59	62.1	1147	1 S47647	nitric-oxide synth
4	59	62.1	1147	1 S38253	nitric-oxide synth
5	59	62.1	1147	1 I53165	nitric-oxide synth
6	59	62.1	1147	2 JC5027	nitric-oxide synth
7	55	57.9	1147	1 I56575	nitric-oxide synth
8	55	57.9	1147	2 JC5028	nitric-oxide synth
9	55	57.9	1147	2 JC5028	nitric-oxide synth
10	55	57.9	1147	2 S65440	nitric-oxide synth
11	49	51.6	1217	2 F69823	probable phosphos
12	48	50.5	1203	1 A47501	nitric-oxide synth
13	47	49.5	386	2 E84562	ATP-dependent prot
14	47	49.5	748	2 E86694	probable tub famil
15	47	49.5	842	2 T34902	clp proteinase Atp
16	47	49.5	1205	1 A38943	nitric-oxide synth
17	46	48.4	741	2 D75500	ATP-dependent Clp
18	46	48.4	758	2 B83319	ATP-binding protel
19	46	48.4	791	2 H72258	endopeptidase Clp
20	46	48.4	856	1 F64098	endopeptidase Clp
21	46	48.4	859	2 F81863	ClpB protein NMA16
22	46	48.4	859	2 F81078	clpB protein NMB14
23	46	48.4	861	2 D82814	ATP-dependent Clp
24	46	48.4	2290	1 GNNYE	genome polyprotein
25	46	48.4	2292	1 GNNYE	genome polyprotein
26	46	48.4	2292	1 GNNYE	genome polyprotein
27	46	48.4	2292	2 S35961	capsid polyprotein
28	46	48.4	2292	2 S55401	capsid polyprotein
29	45.5	47.9	369	2 E70743	probable murB prot

ALIGNMENTS

RESULT 1

A49676  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 20-Jun-2000  
C:Accession: A49676; JX0345; G01947; I38933; S47566; A47475  
R:Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; Hall, V.S.;  
Proc. Natl. Acad. Sci. U.S.A. 90, 11419-11423, 1993  
A:Title: Cloning, characterization, and expression of a cDNA encoding an inducible ni  
A:Reference number: A49676; MUID:94068614  
A:Accession: A49676  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1153 <RES>  
A:Cross-references: EMBL:X73029; NID:g441452; PIDN:CAA51512.1; PID:g441453  
R:Hokari, A.; Zeniya, M.; Esumi, H.  
J. Biochem. 116, 575-581, 1994  
A:Title: Cloning and functional expression of human inducible nitric oxide synthase (A  
A:Reference number: JX0345; MUID:95155267  
A:Accession: JX0345  
A:Molecule type: mRNA  
A:Residues: 1-607, 'L', 609-1153 <HOK>  
A:Cross-references: DBJ:D26525; NID:g559326; PIDN:BAA05531.1; PID:g1228940  
R:Park, C.; Park, R.; Krishna, G.  
submitted to the EMBL Data Library, July 1995  
A:Reference number: G08912  
A:Accession: G01947  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-607, 'L', 609-1153 <PAR>  
A:Cross-references: EMBL:U31511; NID:g951320; PIDN:AAB49041.1; PID:g951321  
R:Guo, F.H.; De Raeye, H.R.; Rice, T.W.; Stuehr, D.J.; Thunnissen, F.B.; Erzurum, S.C  
Proc. Natl. Acad. Sci. U.S.A. 92, 7809-7813, 1995  
A:Title: Continuous nitric oxide synthesis by inducible nitric oxide synthase in norm  
A:Reference number: I38933; MUID:95372368  
A:Accession: I38933  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-675, 'I', 677-932, 'G', 934-965, 'A', 967-1153 <RE2>  
A:Cross-references: EMBL:U20141; NID:g687680; PIDN:AAB60366.1; PID:g687681  
R:Maier, R.; Bilbe, G.; Rediske, J.; Lotz, M.  
Biochim. Biophys. Acta 1208, 145-150, 1994  
A:Title: Inducible nitric oxide synthase from human articular chondrocytes: cDNA clon  
A:Reference number: S47566; MUID:94368816  
A:Accession: S47566  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-22, 'G', 24-153, 'L', 155-176, 'V', 178-799, 'A', 801-912, 'P', 914-1153 <MAI>  
A:Cross-references: EMBL:U05810; NID:g452487; PIDN:AAA56666.1; PID:g452488  
R:Geller, D.A.; Lowenstein, C.J.; Shapiro, R.A.; Nussler, A.K.; Di Silvio, M.; Wang,  
Proc. Natl. Acad. Sci. U.S.A. 90, 3491-3495, 1993

ATP-dependent prot  
ClpB protein PA454  
endopeptidase Clp  
heat shock protein  
D-3-phosphoglycerate  
heat shock protein  
probable two-compo  
conserved hypothet  
probable oxidase,  
sarcosine oxidase,  
probable hexosyltr  
hypothetical ABC t  
hypothetical prote  
cytoskeletal prote  
endopeptidase Clp,  
probable endopepti

A:Title: Molecular cloning and expression of inducible nitric oxide synthase from human  
A:Reference number: A47475; MUID:93234523  
A:Accession: A47475  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-422, 'V', 424-804, 'D', 806-830, 'SP', 833-932, 'G', 934-965, 'A', 967-986, 'V', 988-1144  
A:Cross-references: GB:L09210; NID:g292241; PIDN:AAA59171.1; PID:g292242  
A:Experimental source: hepatocytes  
A>Note: sequence extracted from NCBI backbone (NCBIP:129733)  
C:Genetics:  
A:Gene: GDB:NOS2A; NOS2; INOS  
A:Cross-references: GDB:139215; OMIM:163730  
A:Map position: 17cen-17q11.2  
C:Function:  
A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH  
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reductase  
C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal  
F:509-529/Region: calmodulin binding #status predicted  
F:539-1127/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
F:541-677/Domain: flavodoxin homology <FLX>  
F:623-654/Region: FMN binding #status predicted  
F:765-778/Region: FAD-pyrophosphate binding #status predicted  
F:903-913/Region: FAD-isoxanthine binding #status predicted  
F:978-996/Region: NADP-ribose binding #status predicted  
F:1076-1091/Region: NADP-adenine binding #status predicted  
F:1200/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.08; Score 95; DB 2; Length 1153;  
Best Local Similarity 100.08; Pred. No. 2.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVOGILERVVDGPTPH 18  
|||||

Db 781 PALVOGILERVVDGPTPH 798  
|||||

RESULT 2  
A43271  
nitric-oxide synthase (EC 1.14.13.39), calmodulin-independent - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Mar-2000  
A:Accession: A43271; A42166; JN0458; A46186  
R:Xie, O.; Cho, H.J.; Calaycay, J.; Mumford, R.A.; Swiderek, K.M.; Lee, T.D.; Ding, A.; Science 256, 225-228, 1992  
A:Title: Cloning and characterization of inducible nitric oxide synthase from mouse macrophages  
A:Reference number: A43271; MUID:92229444  
A:Accession: A43271  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1144 <XTE>  
A:Cross-references: GB:M87039; NID:g198406; PIDN:AAA39315.1; PID:g198407  
R:Lyon, C.R.; Orloff, G.J.; Cunningham, J.M.  
J. Biol. Chem. 267, 6370-6374, 1992  
A:Title: Molecular cloning and functional expression of an inducible nitric oxide synthase from mouse macrophages  
A:Reference number: A42166; MUID:92210618  
A:Accession: A42166  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1144 <LYO>  
A:Cross-references: GB:M84373; NID:g200095; PIDN:AAA39834.1; PID:g200096  
R:Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.  
Biochem. Biophys. Res. Commun. 191, 767-774, 1993  
A:Title: Hepatocytes and macrophages express an identical cytokine inducible nitric oxide synthase  
A:Reference number: JN0457; MUID:93221515  
A:Accession: JN0458  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-278, 'F', 280-682, 'H', 684-937, 939-1144 <WOO>  
A:Experimental source: liver  
R:Lowenstein, C.J.; Glatt, C.S.; Bredt, D.S.; Snyder, S.H.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6711-6715, 1992  
A:Title: Cloned and expressed macrophage nitric oxide synthase contrasts with the brain

A:Reference number: A46186; MUID:92357701  
A:Accession: A46186  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-190, 'V', 192-765, 'P', 767-843, 'G', 845-1144 <LOW>  
A:Cross-references: GB:M92649; NID:g200109  
A:Experimental source: BALB/c, RAW 264.7 cells, macrophage  
A>Note: sequence extracted from NCBI backbone (NCBIP:113541)  
C:Genetics:  
A:Gene: NOS  
C:Function:  
A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NAD  
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reductase  
C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me  
F:533-1121/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
F:535-671/Domain: flavodoxin homology <FLX>  
F:194/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 83.2%; Score 79; DB 1; Length 1144;  
Best Local Similarity 94.1%; Pred. No. 9.3e-05;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ALVOGILERVVDGPTPH 18  
|||||

Db 776 ALVOGILERVVDGPTPH 792  
|||||

RESULT 3  
S47647  
nitric-oxide synthase (EC 1.14.13.39) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 16-Jun-2000  
C:Accession: S47647; JCI472  
R:Geng, Y.; Almqvist, M.; Hansson, G.K.  
Biochim. Biophys. Acta 1218, 421-424, 1994  
A:Title: cDNA cloning and expression of inducible nitric oxide synthase from rat vascular smooth muscle cells  
A:Reference number: S47647; MUID:94325351  
A:Accession: S47647  
A:Molecule type: mRNA  
A:Residues: 1-1147 <GEN>  
A:Cross-references: EMBL:X76881; NID:g439283; PIDN:CAA54208.1; PID:g439284  
R:Nunokawa, Y.; Ishida, N.; Tanaka, S.  
Biochem. Biophys. Res. Commun. 191, 89-94, 1993  
A:Title: Cloning of inducible nitric oxide synthase in rat vascular smooth muscle cells  
A:Reference number: JCI472; MUID:93191721  
A:Accession: JCI472  
A:Molecule type: DNA  
A:Residues: 1-71, 'Y', 73-347, 'PV', 350-678, 'VP', 681-720, 'L', 722-739, 'L', 741-843, 'G', 845  
A:Cross-references: DBJ:D14051; NID:g286260; PIDN:BAA03138.1; PID:g286261  
A:Experimental source: vascular smooth muscle  
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reductase  
C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me  
F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
F:538-674/Domain: flavodoxin homology <FLX>  
F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 62.1%; Score 59; DB 1; Length 1147;  
Best Local Similarity 81.2%; Pred. No. 0.2;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALVOGILERVVDGPTPH 17  
|||||

Db 779 ALVOGILERVVDGPTPH 794  
|||||

RESULT 4  
S38253  
nitric-oxide synthase (EC 1.14.13.39) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 16-Jun-2000  
C:Accession: S38253; JN0457

R;Adachi, H.; Iida, S.; Ouchi, S.; Ohshima, H.; Suzuki, H.; Nagasaki, K.; Kawasaki, H.; Eur. J. Biochem. 217, 37-43, 1993  
 A:Title: Molecular cloning of a cDNA encoding an inducible calmodulin-dependent nitric-oxide synthase from rat liver  
 A:Reference number: S38253; MUID:94039059  
 A:Accession: S38253  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <RES>  
 A:Cross-references: GB:D12520; NID:G391858; PIDN:BAA02090.1; PID:G391859  
 A:Experimental source: liver  
 R;Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G. Biochem. Biophys. Res. Commun. 191, 767-774, 1993  
 A:Title: Hepatocytes and macrophages express an identical cytokine inducible nitric oxide synthase  
 A:Reference number: JN0457; MUID:93221515  
 A:Accession: JN0457  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-41, 'SS', '44-103, 105-190, 'Q', 192-213, 'R', 215-247, 'P', 249-263, 'I', 265-373, 'IE', 'S', 896-1000, 'LG', 1003-1015, 'RR', 1018-1026, 'EQ', 1029-1147 <WOO>  
 A:Cross-references: PIDN:AB26037.1  
 A:Experimental source: liver  
 C:Genetics: NOS  
 C:Function: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reductase  
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted  
 A:Gene: NOS  
 Query Match 62.1%; Score 59; DB 1; Length 1147;  
 Best Local Similarity 81.2%; Pred. No. 0.2;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALVQILERVVDGTP 17  
 |||||  
 Db 779 ALVQILERVVDGSSP 794

RESULT 5  
 I53165  
 nitric-oxide synthase (EC 1.14.13.39) [similarity] - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 05-May-2000  
 C:Accession: I53165  
 R;Karlsen, A.E.; Andersen, H.U.; Vissing, H.; Larsen, P.M.; Fey, S.J.; Cuartero, B.G.; Madsen, J. Diabetes 44, 753-758, 1995  
 A:Title: Cloning and expression of cytokine-inducible nitric oxide synthase cDNA from rat liver  
 A:Reference number: I53165; MUID:95309542  
 A:Accession: I53165  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <RES>  
 A:Cross-references: EMBL:U26686; NID:G886072; PIDN:AA85861.1; PID:G886073  
 C:Genetics: NOS  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reductase  
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted  
 Query Match 62.1%; Score 59; DB 1; Length 1147;  
 Best Local Similarity 81.2%; Pred. No. 0.2;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALVQILERVVDGTP 17  
 |||||  
 Db 779 ALVQILERVVDGSSP 794

RESULT 6  
 JC5027  
 nitric-oxide synthase (EC 1.14.13.39) K - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 21-Jan-1997 #sequence\_revision 21-Jan-1997 #text\_change 20-Jun-2000  
 C:Accession: JC5027  
 R;Tsutsunishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa Biol. Pharm. Bull. 19, 1374-1376, 1996  
 A:Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and spleen  
 A:Reference number: JC5027; MUID:97070590  
 A:Accession: JC5027  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <TSU>  
 A:Cross-references: DBJ:D83661; NID:G1209382; PIDN:BAA12035.1; PID:G1853973  
 A:Experimental source: kidney  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reductase  
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal  
 F:191-199/Domain: heme-binding #status predicted <HMB>  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:620-647/Domain: FMN binding #status predicted <FMN>  
 F:764-775, 899-910/Domain: FAD binding #status predicted <FAD>  
 F:975-993, 1034-1067/Domain: NADP binding #status predicted <NDP>  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted  
 Query Match 62.1%; Score 59; DB 2; Length 1147;  
 Best Local Similarity 81.2%; Pred. No. 0.2;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALVQILERVVDGTP 17  
 |||||  
 Db 779 ALVQILERVVDGSSP 794

RESULT 7  
 I56575  
 nitric-oxide synthase (EC 1.14.13.39) [similarity] - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 05-May-2000  
 C:Accession: I56575  
 R;Galea, E.; Reis, D.J.; Feinstein, D.L. J. Neurosci. Res. 37, 406-414, 1994  
 A:Title: Cloning and expression of inducible nitric oxide synthase from rat astrocyte  
 A:Reference number: I56575; MUID:94231594  
 A:Accession: I56575  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <RES>  
 A:Cross-references: EMBL:U03699; NID:G430718; PIDN:AA013747.1; PID:G430719  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reductase  
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted  
 Query Match 57.9%; Score 55; DB 1; Length 1147;  
 Best Local Similarity 80.0%; Pred. No. 0.91;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVQGILERVVDGTP 17  
 |||||  
 Db 780 LVQGILERVVDGSSP 794

RESULT 8  
 JC5028  
 nitric-oxide synthase (EC 1.14.13.39) L - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 04-Mar-2000  
 C:Accession: JC5028

R:Tsutsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, M  
 Biol. Pharm. Bull. 19, 1374-1376, 1996  
 A>Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and u  
 A:Reference number: JC5027; MUID:97070590  
 A:Accession: JC5028  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <TSU>  
 A:Experimental source: lung  
 C:Comment: This protein synthesizes nitric oxide from L-arginine.  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reduc  
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 57.9%; Score 55; DB 2; Length 1147;  
 Best Local Similarity 80.0%; Pred. No. 0.91;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVQGLERVVDGPTP 17  
 |||||  
 Db 780 LVQGLERVVDGSSP 794

RESULT 9  
 JC5029  
 nitric-oxide synthase (EC 1.14.13.39) U - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 04-Mar-2000  
 C:Accession: JC5029  
 R:Tsutsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, M  
 Biol. Pharm. Bull. 19, 1374-1376, 1996  
 A>Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and u  
 A:Reference number: JC5027; MUID:97070590  
 A:Accession: JC5029  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <TSU>  
 A:Experimental source: uterus  
 C:Comment: This protein synthesizes nitric oxide from L-arginine.  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reduc  
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 57.9%; Score 55; DB 2; Length 1147;  
 Best Local Similarity 80.0%; Pred. No. 0.91;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVQGLERVVDGPTP 17  
 |||||  
 Db 780 LVQGLERVVDGSSP 794

RESULT 10  
 S65440  
 nitric-oxide synthase (EC 1.14.13.39) - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 04-Mar-2000  
 A:Accession: S65440  
 R:Iwashina, M.; Hirata, Y.; Imai, T.; Sato, K.; Marumo, F.  
 Eur. J. Biochem. 237, 668-673, 1996  
 A>Title: Molecular cloning of endothelial, inducible nitric oxide synthase gene from rat  
 A:Reference number: S65440; MUID:96235231  
 A:Accession: S65440  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <IWA>  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reduc

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me  
 F:506-535/Region: calmodulin binding  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:599-618/Region: biopterin binding  
 F:620-647/Region: FMN binding #status predicted  
 F:764-775/Region: FAD binding #status predicted  
 F:901-910/Region: FAD binding #status predicted  
 F:975-993/Region: NADPH binding #status predicted  
 F:1074-1087/Region: NADPH binding #status predicted  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 57.9%; Score 55; DB 2; Length 1147;  
 Best Local Similarity 100.0%; Pred. No. 0.91;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALVQGLERVVD 13  
 |||||  
 Db 779 ALVQGLERVVD 790

RESULT 11  
 F69823  
 probable phosphoesterase (EC 3.1.-.-) yhcR - Bacillus subtilis  
 N:Alternate names: 5'-nucleotidase homolog yhcR  
 C:Species: Bacillus subtilis  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 24-Sep-1999  
 C:Accession: F69823  
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber  
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;  
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,  
 Nature 390, 249-256, 1997  
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gal  
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M  
 Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino  
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau  
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl  
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se  
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya  
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
 A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili  
 A:Reference number: A69580; MUID:98044033  
 A:Accession: F69823  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1217 <KUN>  
 A:Cross-references: GB:299108; GB:AL009126; NID:g2633055; PIDN:CAB12747.1; PID:cl1829  
 A:Experimental source: strain 168  
 C:Comment: This sequence has motifs characteristic of a variety of phosphoesterases.  
 C:Genetics:  
 A:Gene: yhcR  
 C:Superfamily: unassigned probable phosphoesterases; phosphoesterase core homology  
 C:Keywords: hydrolase  
 F:591-682/Domain: phosphoesterase core homology <PEC>

Query Match 51.6%; Score 49; DB 2; Length 1217;  
 Best Local Similarity 64.3%; Pred. No. 9.7;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 QGILERVVDGPTP 18  
 :||:|||||  
 Db 379 EGIVDRVVDGDTIH 392

RESULT 12  
 A47501  
 nitric-oxide synthase (EC 1.14.13.39), endothelial - human  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Jun-1995 #sequence\_revision 21-Jul-1995 #text\_change 03-Mar-2000



C:Accession: A47501; S24052; A38948; A49813; A42867; S45691; I37361  
R:Marsden, P.A.; Heng, H.H.Q.; Scherer, S.W.; Stewart, R.J.; Hall, A.V.; Shi, X.M.; Tsui  
J. Biol. Chem. 268, 17478-17488, 1993  
A:Title: Structure and chromosomal localization of the human constitutive endothelial nitric oxide synthase  
A:Reference number: A47501; MUID:93352539  
A:Accession: A47501  
A:Molecule type: DNA  
A:Residues: 1-1203 <MAR1>  
A:Cross-references: GB:L10709; NID:9348235; PIDN:AAA36365.1; PID:9348237; GB:L10693; NID:0698; NID:9348224; GB:L10699; NID:9348225; GB:L10700; NID:9348226; GB:L10701; NID:9348227  
ID:9348232; GB:L10707; NID:9348233; GB:L10708; NID:9348234  
R:Marsden, P.A.; Schappert, K.T.; Chen, H.S.; Flowers, M.; Sundell, C.L.; Wilcox, J.N.; FEBS Lett. 307, 287-293, 1992  
A:Title: Molecular cloning and characterization of human endothelial nitric oxide synthase  
A:Reference number: S24052; MUID:92354731  
A:Accession: S24052  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1203 <MAR2>  
A:Cross-references: GB:M95296; NID:9189259; PIDN:AAA36372.1; PID:9189260  
R:Janssens, S.P.; Shimouchi, A.; Quettermous, T.; Bloch, D.B.; Bloch, K.D.  
submitted to GenBank, September 1992  
A:Reference number: A38948  
A:Accession: A38948  
A:Molecule type: mRNA  
A:Residues: 1-1203 <JAN1>  
A:Cross-references: GB:M93718; NID:9189211; PIDN:AAA36364.1; PID:9189212  
A:Note: the sequence in GenBank entry HUMNIOXSYN, release 111.0, has been corrected to C  
R:Janssens, S.P.; Shimouchi, A.; Quettermous, T.; Bloch, D.B.; Bloch, K.D.  
J. Biol. Chem. 267, 22694b, 1992  
A:Reference number: A49813; MUID:93054573  
A:Contents: erratum  
A:Accession: A49813  
A:Molecule type: mRNA  
A:Residues: 1191-1203 <JAN2>  
A:Cross-references: PIDN:AAB23920.1; PID:9258793  
A:Note: sequence extracted from NCBI backbone (NCBIP:117314)  
R:Janssens, S.P.; Shimouchi, A.; Quettermous, T.; Bloch, D.B.; Bloch, K.D.  
J. Biol. Chem. 267, 14519-14522, 1992  
A:Title: Cloning and expression of a cDNA encoding human endothelium-derived relaxing factor  
A:Reference number: A42867; MUID:92340475  
A:Accession: A42867  
A:Molecule type: mRNA  
A:Residues: 1-82, 'S', '84-179, 'F', 181-566, 'W', 568-647, 'Q', 649-854, 'V', 856-1008, 'G', 1010-1110, 'P', 1111-1112, 'S', 1113-1114, 'S', 1115-1116, 'S', 1117-1118, 'S', 1119-1120, 'S', 1121-1122, 'S', 1123-1124, 'S', 1125-1126, 'S', 1127-1128, 'S', 1129-1130, 'S', 1131-1132, 'S', 1133-1134, 'S', 1135-1136, 'S', 1137-1138, 'S', 1139-1140, 'S', 1141-1142, 'S', 1143-1144, 'S', 1145-1146, 'S', 1147-1148, 'S', 1149-1150, 'S', 1151-1152, 'S', 1153-1154, 'S', 1155-1156, 'S', 1157-1158, 'S', 1159-1160, 'S', 1161-1162, 'S', 1163-1164, 'S', 1165-1166, 'S', 1167-1168, 'S', 1169-1170, 'S', 1171-1172, 'S', 1173-1174, 'S', 1175-1176, 'S', 1177-1178, 'S', 1179-1180, 'S', 1181-1182, 'S', 1183-1184, 'S', 1185-1186, 'S', 1187-1188, 'S', 1189-1190, 'S', 1191-1192, 'S', 1193-1194, 'S', 1195-1196, 'S', 1197-1198, 'S', 1199-1200, 'S', 1201-1202, 'S', 1203-1204, 'S', 1205-1206, 'S', 1207-1208, 'S', 1209-1210, 'S', 1211-1212, 'S', 1213-1214, 'S', 1215-1216, 'S', 1217-1218, 'S', 1219-1220, 'S', 1221-1222, 'S', 1223-1224, 'S', 1225-1226, 'S', 1227-1228, 'S', 1229-1230, 'S', 1231-1232, 'S', 1233-1234, 'S', 1235-1236, 'S', 1237-1238, 'S', 1239-1240, 'S', 1241-1242, 'S', 1243-1244, 'S', 1245-1246, 'S', 1247-1248, 'S', 1249-1250, 'S', 1251-1252, 'S', 1253-1254, 'S', 1255-1256, 'S', 1257-1258, 'S', 1259-1260, 'S', 1261-1262, 'S', 1263-1264, 'S', 1265-1266, 'S', 1267-1268, 'S', 1269-1270, 'S', 1271-1272, 'S', 1273-1274, 'S', 1275-1276, 'S', 1277-1278, 'S', 1279-1280, 'S', 1281-1282, 'S', 1283-1284, 'S', 1285-1286, 'S', 1287-1288, 'S', 1289-1290, 'S', 1291-1292, 'S', 1293-1294, 'S', 1295-1296, 'S', 1297-1298, 'S', 1299-1300, 'S', 1301-1302, 'S', 1303-1304, 'S', 1305-1306, 'S', 1307-1308, 'S', 1309-1310, 'S', 1311-1312, 'S', 1313-1314, 'S', 1315-1316, 'S', 1317-1318, 'S', 1319-1320, 'S', 1321-1322, 'S', 1323-1324, 'S', 1325-1326, 'S', 1327-1328, 'S', 1329-1330, 'S', 1331-1332, 'S', 1333-1334, 'S', 1335-1336, 'S', 1337-1338, 'S', 1339-1340, 'S', 1341-1342, 'S', 1343-1344, 'S', 1345-1346, 'S', 1347-1348, 'S', 1349-1350, 'S', 1351-1352, 'S', 1353-1354, 'S', 1355-1356, 'S', 1357-1358, 'S', 1359-1360, 'S', 1361-1362, 'S', 1363-1364, 'S', 1365-1366, 'S', 1367-1368, 'S', 1369-1370, 'S', 1371-1372, 'S', 1373-1374, 'S', 1375-1376, 'S', 1377-1378, 'S', 1379-1380, 'S', 1381-1382, 'S', 1383-1384, 'S', 1385-1386, 'S', 1387-1388, 'S', 1389-1390, 'S', 1391-1392, 'S', 1393-1394, 'S', 1395-1396, 'S', 1397-1398, 'S', 1399-1400, 'S', 1401-1402, 'S', 1403-1404, 'S', 1405-1406, 'S', 1407-1408, 'S', 1409-1410, 'S', 1411-1412, 'S', 1413-1414, 'S', 1415-1416, 'S', 1417-1418, 'S', 1419-1420, 'S', 1421-1422, 'S', 1423-1424, 'S', 1425-1426, 'S', 1427-1428, 'S', 1429-1430, 'S', 1431-1432, 'S', 1433-1434, 'S', 1435-1436, 'S', 1437-1438, 'S', 1439-1440, 'S', 1441-1442, 'S', 1443-1444, 'S', 1445-1446, 'S', 1447-1448, 'S', 1449-1450, 'S', 1451-1452, 'S', 1453-1454, 'S', 1455-1456, 'S', 1457-1458, 'S', 1459-1460, 'S', 1461-1462, 'S', 1463-1464, 'S', 1465-1466, 'S', 1467-1468, 'S', 1469-1470, 'S', 1471-1472, 'S', 1473-1474, 'S', 1475-1476, 'S', 1477-1478, 'S', 1479-1480, 'S', 1481-1482, 'S', 1483-1484, 'S', 1485-1486, 'S', 1487-1488, 'S', 1489-1490, 'S', 1491-1492, 'S', 1493-1494, 'S', 1495-1496, 'S', 1497-1498, 'S', 1499-1500, 'S', 1501-1502, 'S', 1503-1504, 'S', 1505-1506, 'S', 1507-1508, 'S', 1509-1510, 'S', 1511-1512, 'S', 1513-1514, 'S', 1515-1516, 'S', 1517-1518, 'S', 1519-1520, 'S', 1521-1522, 'S', 1523-1524, 'S', 1525-1526, 'S', 1527-1528, 'S', 1529-1530, 'S', 1531-1532, 'S', 1533-1534, 'S', 1535-1536, 'S', 1537-1538, 'S', 1539-1540, 'S', 1541-1542, 'S', 1543-1544, 'S', 1545-1546, 'S', 1547-1548, 'S', 1549-1550, 'S', 1551-1552, 'S', 1553-1554, 'S', 1555-1556, 'S', 1557-1558, 'S', 1559-1560, 'S', 1561-1562, 'S', 1563-1564, 'S', 1565-1566, 'S', 1567-1568, 'S', 1569-1570, 'S', 1571-1572, 'S', 1573-1574, 'S', 1575-1576, 'S', 1577-1578, 'S', 1579-1580, 'S', 1581-1582, 'S', 1583-1584, 'S', 1585-1586, 'S', 1587-1588, 'S', 1589-1590, 'S', 1591-1592, 'S', 1593-1594, 'S', 1595-1596, 'S', 1597-1598, 'S', 1599-1600, 'S', 1601-1602, 'S', 1603-1604, 'S', 1605-1606, 'S', 1607-1608, 'S', 1609-1610, 'S', 1611-1612, 'S', 1613-1614, 'S', 1615-1616, 'S', 1617-1618, 'S', 1619-1620, 'S', 1621-1622, 'S', 1623-1624, 'S', 1625-1626, 'S', 1627-1628, 'S', 1629-1630, 'S', 1631-1632, 'S', 1633-1634, 'S', 1635-1636, 'S', 1637-1638, 'S', 1639-1640, 'S', 1641-1642, 'S', 1643-1644, 'S', 1645-1646, 'S', 1647-1648, 'S', 1649-1650, 'S', 1651-1652, 'S', 1653-1654, 'S', 1655-1656, 'S', 1657-1658, 'S', 1659-1660, 'S', 1661-1662, 'S', 1663-1664, 'S', 1665-1666, 'S', 1667-1668, 'S', 1669-1670, 'S', 1671-1672, 'S', 1673-1674, 'S', 1675-1676, 'S', 1677-1678, 'S', 1679-1680, 'S', 1681-1682, 'S', 1683-1684, 'S', 1685-1686, 'S', 1687-1688, 'S', 1689-1690, 'S', 1691-1692, 'S', 1693-1694, 'S', 1695-1696, 'S', 1697-1698, 'S', 1699-1700, 'S', 1701-1702, 'S', 1703-1704, 'S', 1705-1706, 'S', 1707-1708, 'S', 1709-1710, 'S', 1711-1712, 'S', 1713-1714, 'S', 1715-1716, 'S', 1717-1718, 'S', 1719-1720, 'S', 1721-1722, 'S', 1723-1724, 'S', 1725-1726, 'S', 1727-1728, 'S', 1729-1730, 'S', 1731-1732, 'S', 1733-1734, 'S', 1735-1736, 'S', 1737-1738, 'S', 1739-1740, 'S', 1741-1742, 'S', 1743-1744, 'S', 1745-1746, 'S', 1747-1748, 'S', 1749-1750, 'S', 1751-1752, 'S', 1753-1754, 'S', 1755-1756, 'S', 1757-1758, 'S', 1759-1760, 'S', 1761-1762, 'S', 1763-1764, 'S', 1765-1766, 'S', 1767-1768, 'S', 1769-1770, 'S', 1771-1772, 'S', 1773-1774, 'S', 1775-1776, 'S', 1777-1778, 'S', 1779-1780, 'S', 1781-1782, 'S', 1783-1784, 'S', 1785-1786, 'S', 1787-1788, 'S', 1789-1790, 'S', 1791-1792, 'S', 1793-1794, 'S', 1795-1796, 'S', 1797-1798, 'S', 1799-1800, 'S', 1801-1802, 'S', 1803-1804, 'S', 1805-1806, 'S', 1807-1808, 'S', 1809-1810, 'S', 1811-1812, 'S', 1813-1814, 'S', 1815-1816, 'S', 1817-1818, 'S', 1819-1820, 'S', 1821-1822, 'S', 1823-1824, 'S', 1825-1826, 'S', 1827-1828, 'S', 1829-1830, 'S', 1831-1832, 'S', 1833-1834, 'S', 1835-1836, 'S', 1837-1838, 'S', 1839-1840, 'S', 1841-1842, 'S', 1843-1844, 'S', 1845-1846, 'S', 1847-1848, 'S', 1849-1850, 'S', 1851-1852, 'S', 1853-1854, 'S', 1855-1856, 'S', 1857-1858, 'S', 1859-1860, 'S', 1861-1862, 'S', 1863-1864, 'S', 1865-1866, 'S', 1867-1868, 'S', 1869-1870, 'S', 1871-1872, 'S', 1873-1874, 'S', 1875-1876, 'S', 1877-1878, 'S', 1879-1880, 'S', 1881-1882, 'S', 1883-1884, 'S', 1885-1886, 'S', 1887-1888, 'S', 1889-1890, 'S', 1891-1892, 'S', 1893-1894, 'S', 1895-1896, 'S', 1897-1898, 'S', 1899-1900, 'S', 1901-1902, 'S', 1903-1904, 'S', 1905-1906, 'S', 1907-1908, 'S', 1909-1910, 'S', 1911-1912, 'S', 1913-1914, 'S', 1915-1916, 'S', 1917-1918, 'S', 1919-1920, 'S', 1921-1922, 'S', 1923-1924, 'S', 1925-1926, 'S', 1927-1928, 'S', 1929-1930, 'S', 1931-1932, 'S', 1933-1934, 'S', 1935-1936, 'S', 1937-1938, 'S', 1939-1940, 'S', 1941-1942, 'S', 1943-1944, 'S', 1945-1946, 'S', 1947-1948, 'S', 1949-1950, 'S', 1951-1952, 'S', 1953-1954, 'S', 1955-1956, 'S', 1957-1958, 'S', 1959-1960, 'S', 1961-1962, 'S', 1963-1964, 'S', 1965-1966, 'S', 1967-1968, 'S', 1969-1970, 'S', 1971-1972, 'S', 1973-1974, 'S', 1975-1976, 'S', 1977-1978, 'S', 1979-1980, 'S', 1981-1982, 'S', 1983-1984, 'S', 1985-1986, 'S', 1987-1988, 'S', 1989-1990, 'S', 1991-1992, 'S', 1993-1994, 'S', 1995-1996, 'S', 1997-1998, 'S', 1999-2000, 'S', 2001-2002, 'S', 2003-2004, 'S', 2005-2006, 'S', 2007-2008, 'S', 2009-2010, 'S', 2011-2012, 'S', 2013-2014, 'S', 2015-2016, 'S', 2017-2018, 'S', 2019-2020, 'S', 2021-2022, 'S', 2023-2024, 'S', 2025-2026, 'S', 2027-2028, 'S', 2029-2030, 'S', 2031-2032, 'S', 2033-2034, 'S', 2035-2036, 'S', 2037-2038, 'S', 2039-2040, 'S', 2041-2042, 'S', 2043-2044, 'S', 2045-2046, 'S', 2047-2048, 'S', 2049-2050, 'S', 2051-2052, 'S', 2053-2054, 'S', 2055-2056, 'S', 2057-2058, 'S', 2059-2060, 'S', 2061-2062, 'S', 2063-2064, 'S', 2065-2066, 'S', 2067-2068, 'S', 2069-2070, 'S', 2071-2072, 'S', 2073-2074, 'S', 2075-2076, 'S', 2077-2078, 'S', 2079-2080, 'S', 2081-2082, 'S', 2083-2084, 'S', 2085-2086, 'S', 2087-2088, 'S', 2089-2090, 'S', 2091-2092, 'S', 2093-2094, 'S', 2095-2096, 'S', 2097-2098, 'S', 2099-2100, 'S', 2101-2102, 'S', 2103-2104, 'S', 2105-2106, 'S', 2107-2108, 'S', 2109-2110, 'S', 2111-2112, 'S', 2113-2114, 'S', 2115-2116, 'S', 2117-2118, 'S', 2119-2120, 'S', 2121-2122, 'S', 2123-2124, 'S', 2125-2126, 'S', 2127-2128, 'S', 2129-2130, 'S', 2131-2132, 'S', 2133-2134, 'S', 2135-2136, 'S', 2137-2138, 'S', 2139-2140, 'S', 2141-2142, 'S', 2143-2144, 'S', 2145-2146, 'S', 2147-2148, 'S', 2149-2150, 'S', 2151-2152, 'S', 2153-2154, 'S', 2155-2156, 'S', 2157-2158, 'S', 2159-2160, 'S', 2161-2162, 'S', 2163-2164, 'S', 2165-2166, 'S', 2167-2168, 'S', 2169-2170, 'S', 2171-2172, 'S', 2173-2174, 'S', 2175-2176, 'S', 2177-2178, 'S', 2179-2180, 'S', 2181-2182, 'S', 2183-2184, 'S', 2185-2186, 'S', 2187-2188, 'S', 2189-2190, 'S', 2191-2192, 'S', 2193-2194, 'S', 2195-2196, 'S', 2197-2198, 'S', 2199-2200, 'S', 2201-2202, 'S', 2203-2204, 'S', 2205-2206, 'S', 2207-2208, 'S', 2209-2210, 'S', 2211-2212, 'S', 2213-2214, 'S', 2215-2216, 'S', 2217-2218, 'S', 2219-2220, 'S', 2221-2222, 'S', 2223-2224, 'S', 2225-2226, 'S', 2227-2228, 'S', 2229-2230, 'S', 2231-2232, 'S', 2233-2234, 'S', 2235-2236, 'S', 2237-2238, 'S', 2239-2240, 'S', 2241-2242, 'S', 2243-2244, 'S', 2245-2246, 'S', 2247-2248, 'S', 2249-2250, 'S', 2251-2252, 'S', 2253-2254, 'S', 2255-2256, 'S', 2257-2258, 'S', 2259-2260, 'S', 2261-2262, 'S', 2263-2264, 'S', 2265-2266, 'S', 2267-2268, 'S', 2269-2270, 'S', 2271-2272, 'S', 2273-2274, 'S', 2275-2276, 'S', 2277-2278, 'S', 2279-2280, 'S', 2281-2282, 'S', 2283-2284, 'S', 2285-2286, 'S', 2287-2288, 'S', 2289-2290, 'S', 2291-2292, 'S', 2293-2294, 'S', 2295-2296, 'S', 2297-2298, 'S', 2299-2300, 'S', 2301-2302, 'S', 2303-2304, 'S', 2305-2306, 'S', 2307-2308, 'S', 2309-2310, 'S', 2311-2312, 'S', 2313-2314, 'S', 2315-2316, 'S', 2317-2318, 'S', 2319-2320, 'S', 2321-2322, 'S', 2323-2324, 'S', 2325-2326, 'S', 2327-2328, 'S', 2329-2330, 'S', 2331-2332, 'S', 2333-2334, 'S', 2335-2336, 'S', 2337-2338, 'S', 2339-2340, 'S', 2341-2342, 'S', 2343-2344, 'S', 2345-2346, 'S', 2347-2348, 'S', 2349-2350, 'S', 2351-2352, 'S', 2353-2354, 'S', 2355-2356, 'S', 2357-2358, 'S', 2359-2360, 'S', 2361-2362, 'S', 2363-2364, 'S', 2365-2366, 'S', 2367-2368, 'S', 2369-2370, 'S', 2371-2372, 'S', 2373-2374, 'S', 2375-2376, 'S', 2377-2378, 'S', 2379-2380, 'S', 2381-2382, 'S', 2383-2384, 'S', 2385-2386, 'S', 2387-2388, 'S', 2389-2390, 'S', 2391-2392, 'S', 2393-2394, 'S', 2395-2396, 'S', 2397-2398, 'S', 2399-2400, 'S', 2401-2402, 'S', 2403-2404, 'S', 2405-2406, 'S', 2407-2408, 'S', 2409-2410, 'S', 2411-2412, 'S', 2413-2414, 'S', 2415-2416, 'S', 2417-2418, 'S', 2419-2420, 'S', 2421-2422, 'S', 2423-2424, 'S', 2425-2426, 'S', 2427-2428, 'S', 2429-2430, 'S', 2431-2432, 'S', 2433-2434, 'S', 2435-2436, 'S', 2437-2438, 'S', 2439-2440, 'S', 2441-2442, 'S', 2443-2444, 'S', 2445-2446, 'S', 2447-2448, 'S', 2449-2450, 'S', 2451-2452, 'S', 2453-2454, 'S', 2455-2456, 'S', 2457-2458, 'S', 2459-2460, 'S', 2461-2462, 'S', 2463-2464, 'S', 2465-2466, 'S', 2467-2468, 'S', 2469-2470, 'S', 2471-2472, 'S', 2473-2474, 'S', 2475-2476, 'S', 2477-2478, 'S', 2479-2480, 'S', 2481-2482, 'S', 2483-2484, 'S', 2485-2486, 'S', 2487-2488, 'S', 2489-2490, 'S', 2491-2492, 'S', 2493-2494, 'S', 2495-2496, 'S', 2497-2498, 'S', 2499-2500, 'S', 2501-2502, 'S', 2503-2504, 'S', 2505-2506, 'S', 2507-2508, 'S', 2509-2510, 'S', 2511-2512, 'S', 2513-2514, 'S', 2515-2516, 'S', 2517-2518, 'S', 2519-2520, 'S', 2521-2522, 'S', 2523-2524, 'S', 2525-2526, 'S', 2527-2528, 'S', 2529-2530, 'S', 2531-2532, 'S', 2533-2534, 'S', 2535-2536, 'S', 2537-2538, 'S', 2539-2540, 'S', 2541-2542, 'S', 2543-2544, 'S', 2545-2546, 'S', 2547-2548, 'S', 2549-2550, 'S', 2551-2552, 'S', 2553-2554, 'S', 2555-2556, 'S', 2557-2558, 'S', 2559-2560, 'S', 2561-2562, 'S', 2563-2564, 'S', 2565-2566, 'S', 2567-2568, 'S', 2569-2570, 'S', 2571-2572, 'S', 2573-2574, 'S', 2575-2576, 'S', 2577-2578, 'S', 2579-2580, 'S', 2581-2582, 'S', 2583-2584, 'S', 2585-2586, 'S', 2587-2588, 'S', 2589-2590, 'S', 2591-2592, 'S', 2593-2594, 'S', 2595-2596, 'S', 2597-2598, 'S', 2599-2600, 'S', 2601-2602, 'S', 2603-2604, 'S', 2605-2606, 'S', 2607-2608, 'S', 2609-2610, 'S', 2611-2612, 'S', 2613-2614, 'S', 2615-2616, 'S', 2617-2618, 'S', 2619-2620, 'S', 2621-2622, 'S', 2623-2624, 'S', 2625-2626, 'S', 2627-2628, 'S', 2629-2630, 'S', 2631-2632, 'S', 2633-2634, 'S', 2635-2636, 'S', 2637-2638, 'S', 2639-2640, 'S', 2641-2642, 'S', 2643-2644, 'S', 2645-2646, 'S', 2647-2648, 'S', 2649-2650, 'S', 2651-2652, 'S', 2653-2654, 'S', 2655-2656, 'S', 2657-2658, 'S', 2659-2660, 'S', 2661-2662, 'S', 2663-2664, 'S', 2665-2666, 'S', 2667-2668, 'S', 2669-2670, 'S', 2671-2672, 'S', 2673-2674, 'S', 2675-2676, 'S', 2677-2678, 'S',

Query Match 49.5%; Score 47; DB 2; Length 748;  
Best Local Similarity 43.8%; Pred No. 12;  
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 ALVQGILERVVDGTPP 17  
I:|:|:|:|:|  
Db 160 AVVEGLAQKIVDGDVP 175

## RESULT 15

T34902  
Clp protease ATP-binding chain - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 02-Feb-2001  
C:Accession: T34902  
R:Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, June 1998  
A:Reference number: Z21561  
A:Accession: T34902  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-842 <OLI>  
A:Cross-references: EMBL:AL023861; PIDN:CAA19619.1; GSPDB:GN00070; SCOEDB:SC3C8.27c  
A:Experimental source: strain A3(2)  
C:Genetics:

A:Gene: clpA; SCOEDB:SC3C8.27c  
C:Superfamily: endopeptidase Clp ATP-binding chain  
C:Keywords: ATP; molecular chaperone; nucleotide binding; P-loop  
F:235-242/Region: nucleotide-binding motif A (P-loop)  
F:303-308/Region: nucleotide-binding motif B  
F:573-580/Region: nucleotide-binding motif A (P-loop)  
F:641-646/Region: nucleotide-binding motif B  
F:641-646/Region: nucleotide-binding motif B  
F:241/Binding site: ATP (Lys) #status predicted  
F:579/Binding site: ATP (Lys) #status predicted

Query Match 49.5%; Score 47; DB 2; Length 842;  
Best Local Similarity 43.8%; Pred No. 14;  
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 ALVQGILERVVDGTPP 17  
I:|:|:|:|:|  
Db 243 AIVEGLAQKIVDGDVP 258

Search completed: September 10, 2001, 14:01:15  
Job time: 214 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:00:24 ; Search time 67.08 Seconds  
(without alignments)  
16.268 Million cell updates/sec

Title: US-08-833-506c-30

Perfect score: 95  
Sequence: 1 PALVQGLILRVVDGPTPH 18

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	95	100.0	18	AAW81231	Human iNOS peptide
2	95	100.0	18	AAW81179	Human iNOS (781-79)
3	95	100.0	18	AAW81271	Human iNOS peptide
4	95	100.0	18	AAW81276	Human iNOS peptide
5	95	100.0	18	AAW81205	Human iNOS peptide
6	95	100.0	18	AAW81206	Human iNOS peptide
7	95	100.0	18	AAW81209	Human iNOS peptide
8	95	100.0	1146	AAW96322	Inducible nitric o
9	95	100.0	1153	AAW55764	Sequence encoded b
10	95	100.0	1153	AAW63206	Nitric-oxide-synth
11	95	100.0	1153	AAW88464	Hepatocyte inducib

12	95	100.0	1153	19	AAW36113	Human inducible ni
13	95	100.0	1153	22	AAW361724	Amino acid sequenc
14	95	100.0	1153	22	AAW66724	Human inducible ni
15	80	84.2	15	19	AAW81233	Human iNOS peptide
16	80	84.2	15	19	AAW81236	Human iNOS peptide
17	79	83.2	18	19	AAW81180	Mouse iNOS (776-79
18	79	83.2	1144	16	AAW77360	Inducible nitric o
19	79	83.2	1144	19	AAW51246	Human iNOS peptide
20	68	71.6	14	19	AAW81307	Human iNOS peptide
21	68	71.6	14	19	AAW81300	Human iNOS peptide
22	65	68.4	12	19	AAW81234	Human iNOS peptide
23	65	68.4	12	19	AAW81297	Human iNOS peptide
24	59	62.1	1147	17	AAW02571	Rat inducible nitr
25	56	58.9	12	19	AAW81238	Human iNOS peptide
26	56	58.9	12	19	AAW81301	Human iNOS peptide
27	55	57.9	18	19	AAW81181	Rat iNOS (780-794)
28	52	54.7	9	19	AAW81235	Human iNOS peptide
29	52	54.7	9	19	AAW81298	Human iNOS peptide
30	48	50.5	19	19	AAW81232	Human eNOS peptide
31	48	50.5	19	19	AAW81322	Human eNOS peptide
32	48	50.5	1203	14	AAW41668	Human endothelial
33	48	50.5	1203	19	AAW57315	Human endothelial
34	48	50.5	1203	22	AAW31726	Amino acid sequenc
35	48	50.5	1203	22	AAW66726	Human nitric oxide
36	47	49.5	1205	16	AAW77363	Endothelial nitrog
37	47	49.5	1205	17	AAW93930	Bovine endothelial
38	45	47.4	857	20	AAW97702	Staphylococcus aur
39	45	47.4	859	20	AAW29186	Amino acid sequenc
40	44	46.3	70	21	AAW64967	Human 5' EST relat
41	43	45.3	9	19	AAW81239	Human iNOS peptide
42	43	45.3	9	19	AAW81302	Human iNOS peptide
43	43	45.3	45	22	AAW64860	Human secreted pro
44	43	45.3	906	14	AAW30053	E. coli heat shock
45	43	45.3	908	14	AAW33429	E. coli heat shock

#### ALIGNMENTS

RESULT 1

AAW81231	
ID	AAW81231 standard; peptide; 18 AA.
AC	AAW81231:
XX	30-APR-1999 (first entry)
DT	
XX	Human iNOS peptide fragment PS-5166.
DE	
XX	Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW	monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW	myocardial infarction; tissue rejection; transplantation; psoriasis;
KW	autoimmune disease; multiple sclerosis.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 18
FT	/note= "His residue amidated"
XX	
PN	W09845710-AL.
XX	
PD	15-OCT-1998.
XX	
PF	11-APR-1997; 97WO-US066500.
XX	
PR	07-APR-1997; 97US-6667777.
XX	
PA	(WEBB/) WEBBER R.
XX	
PI	Webber R;
XX	
DR	WPI; 1998-594495/50.

XX Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
XX Example 4; Page 36; 93pp; English.  
XX This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathophysiological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
CC invention.  
XX Sequence 18 AA;  
SQ

Query Match 100.0%; Score 95; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.1e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVQGILERVVDGPTPH 18  
Db 1 palvggilervvvdgptph 18  
|||||

RESULT 2  
AAW81179  
ID AAW81179 standard; peptide; 18 AA.  
XX  
AC AAW81179;  
XX  
DT 30-APR-1999 (first entry)  
XX  
DE Human iNOS (781-798) peptide fragment.  
XX  
KW Inducible nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis.  
XX  
OS Homo sapiens.  
XX  
PN WO9845710-A1.  
XX  
PD 15-OCT-1998.  
XX  
PF 11-APR-1997; 97WO-US06500.  
XX  
PR 07-APR-1997; 97US-6667777.  
XX  
PA (WEBB/) WEBBER R.  
XX  
PI Webber R;  
XX  
DR WPI; 1998-594495/50.  
XX  
XX Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
XX Disclosure; Page 20; 93pp; English.  
XX This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and

CC tissues for various pathophysiological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide fragment from human iNOS which is used in the method  
CC of the invention.  
XX Sequence 18 AA;  
SQ

Query Match 100.0%; Score 95; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.1e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVQGILERVVDGPTPH 18  
Db 1 palvggilervvvdgptph 18  
|||||

RESULT 3  
AAW81271  
ID AAW81271 standard; peptide; 18 AA.  
XX  
AC AAW81271;  
XX  
DT 30-APR-1999 (first entry)  
XX  
DE Human iNOS peptide fragment PS-5166.  
XX  
KW Inducible nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 18  
FT /note= "His residue amidated"  
XX  
PN WO9845710-A1.  
XX  
PD 15-OCT-1998.  
XX  
PF 11-APR-1997; 97WO-US06500.  
XX  
PR 07-APR-1997; 97US-6667777.  
XX  
PA (WEBB/) WEBBER R.  
XX  
PI Webber R;  
XX  
DR WPI; 1998-594495/50.  
XX  
XX Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
XX Example 13; Page 55; 93pp; English.  
XX This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathophysiological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
CC invention.  
XX Sequence 18 AA;  
SQ

Query Match 100.0%; Score 95; DB 19; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVQGILERVVDGPTPH 18  
 ||| ||||| ||||| |||||  
 Db 1 palvqgilerervvdgptph 18

RESULT 4  
 AAW81276  
 ID AAW81276 standard; peptide; 18 AA.  
 AC AAW81276;  
 XX  
 XX  
 DT 30-APR-1999 (first entry)  
 XX  
 DE Human iNOS peptide fragment #2.  
 XX  
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
 KW autoimmune disease; multiple sclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO98457110-A1.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PF 11-APR-1997; 97WO-US06500.  
 XX  
 PR 07-APR-1997; 97US-6667777.  
 XX  
 PA (WEBB/) WEBBER R.  
 XX  
 PI Webber R;  
 XX  
 DR WO98457110-A1.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PF 11-APR-1997; 97WO-US06500.  
 XX  
 PR 07-APR-1997; 97US-6667777.  
 XX  
 PA (WEBB/) WEBBER R.  
 XX  
 PI Webber R;  
 XX  
 DR WPI: 1998-594495/50.  
 XX  
 PT Detection of human inducible nitric oxide synthase - using an  
 PT immunoassay in which a sample is contacted with a specific binding  
 PT entity reactive with human iNOS or mimics.  
 XX  
 PS Disclosure; Fig 1; 93pp; English.  
 XX  
 CC This invention describes an immunoassay method where a sample with a  
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
 CC to detect the presence of human iNOS protein in the sample. The method  
 CC can be used for the detection and quantitation of human iNOS in cells and  
 CC tissues for various pathophysiological conditions such as sepsis, septic  
 CC shock, myocardial infarction, rejection of tissue in organs following  
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
 CC represents a peptide from human iNOS which is used in the method of the  
 CC invention.

QY 1 PALVQGILERVVDGPTPH 18  
 ||| ||||| ||||| |||||  
 Db 1 palvqgilerervvdgptph 18

RESULT 5

AAW81205  
 ID AAW81205 standard; peptide; 18 AA.  
 XX  
 AC AAW81205;  
 XX  
 DT 30-APR-1999 (first entry)  
 XX  
 DE Human iNOS peptide fragment capable of binding Mab 2D2-B2.  
 XX  
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
 KW autoimmune disease; multiple sclerosis; Mab.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO98457110-A1.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PF 11-APR-1997; 97WO-US06500.  
 XX  
 PR 07-APR-1997; 97US-6667777.  
 XX  
 PA (WEBB/) WEBBER R.  
 XX  
 PI Webber R;  
 XX  
 DR WPI: 1998-594495/50.  
 XX  
 PT Detection of human inducible nitric oxide synthase - using an  
 PT immunoassay in which a sample is contacted with a specific binding  
 PT entity reactive with human iNOS or mimics.  
 XX  
 PS Example 3; Page 32; 93pp; English.  
 XX  
 CC This invention describes an immunoassay method where a sample with a  
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
 CC to detect the presence of human iNOS protein in the sample. The method  
 CC can be used for the detection and quantitation of human iNOS in cells and  
 CC tissues for various pathophysiological conditions such as sepsis, septic  
 CC shock, myocardial infarction, rejection of tissue in organs following  
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
 CC represents a peptide from human iNOS which is used in the method of the  
 CC invention.

QY 1 PALVQGILERVVDGPTPH 18  
 ||| ||||| ||||| |||||  
 Db 1 palvqgilerervvdgptph 18

RESULT 6  
 AAW81206  
 ID AAW81206 standard; peptide; 18 AA.  
 XX  
 AC AAW81206;  
 XX  
 DT 30-APR-1999 (first entry)  
 XX  
 DE Human iNOS peptide fragment capable of binding Mab 5B3-E6.  
 XX  
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;



PT osteoporosis, inflammatory diseases, autoimmune diseases or  
 PT neurodegenerative diseases  
 XX  
 PS Disclosure; Page 247-251; 253pp; English.

XX Inhibition of cytokine mediated immunotoxicity of cells can be  
 CC achieved by blocking free radical production or the accumulation of  
 CC free radicals in that cell. Treatment of insulin dependent diabetes  
 CC mellitus (IDDM) can be achieved by blocking nitric oxide (NO)  
 CC production in a pancreatic beta cell and by providing a composition  
 CC comprising an agent that reduces levels of fatty acids in the cells  
 CC and protects beta-cells of the subject against lipid-mediated cell  
 CC death. Cells can also be protected against nitric oxide mediated  
 CC cytotoxicity by introducing into the cell an antioxidant agent.  
 CC The methods can be used for protecting cells against immunotoxicity  
 CC mediated by, e.g. IL-1 beta, IL-1 alpha, gamma IFN, TNF alpha, TNF  
 CC beta, IL-8, IL-2, IL-6, IL-3, IL-5, IL-7, IL-9, IL-14, IL-17,  
 CC granulocyte-macrophage colony stimulating factor or monocyte  
 CC chemoattractant protein-1. The methods can be used for the treatment  
 CC of e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity,  
 CC wasting syndromes, short stature, osteoporosis, inflammatory  
 CC diseases, autoimmune diseases, or neurodegenerative diseases.

XX Sequence 1146 AA;

Query Match 100.0%; Score 95; DB 20; Length 1146;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVQGILERVVDGPTPH 18  
 |||||  
 Db 781 palvqgillervvdgptph 798

RESULT 9

AAR55764  
 ID AAR55764 standard; Protein; 1153 AA.

XX  
 AC AAR55764;

XX 28-DEC-1994 (first entry)

XX Sequence encoded by the cDNA clone for human hepatocyte inducible  
 DE nitric oxide synthase.

XX Nitric oxide synthase; hepatocyte; hypotensive shock; therapy.

XX Homo sapiens.

XX WO9412645-A.

PN 09-JUN-1994.

XX 23-NOV-1993; 93WO-US11401.

XX 25-NOV-1992; 92US-0981344.

XX (UYPI-) UNIV PITTSBURGH.

XX Billiar TR, Geller DA, Nussler AK, Simmons RL;

XX WPI; 1994-200273/24.

XX N-PSDB; AAQ66914.

XX cDNA clone encoding human inducible nitric oxide synthase - used  
 PT to prevent the hypotensive shock seen with sepsis.

XX Disclosure; Fig 1; 53pp; English.

XX AAQ66914 is from human hepatocyte inducible nitric oxide synthase cDNA  
 CC clone pHINOS from lambda Zap II cDNA library. The original source  
 CC was induced human hepatocyte RNA. HINOS cDNA plasmid is pref.

CC transformed in E. coli SOLR (ATCC 69126). The inventors claim a  
 CC clone with the cDNA sequence in AAQ66914 and a cDNA clone which  
 CC encodes AAR55764. The cloning and expression of a human tissue nitric  
 CC oxide synthase cDNA provides a source of the enzyme for therapeutic  
 CC purposes, for example to prevent the hypotensive shock seen with  
 CC sepsis.

XX Sequence 1153 AA;

Query Match 100.0%; Score 95; DB 15; Length 1153;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVQGILERVVDGPTPH 18  
 |||||  
 Db 781 palvqgillervvdgptph 798

RESULT 10

AAR63206  
 ID AAR63206 standard; Protein; 1153 AA.

XX  
 AC AAR63206;

XX 09-MAY-1995 (first entry)

XX Nitric-oxide-synthase.

XX Nitric-oxide-synthase; NO-synthase; NOS; chondrocyte;  
 KW interleukin-1 beta; pBSHSINOS; arthritis; hypertension;  
 KW septic shock; inflammation; ischemia; dementia; obesity; tumor;  
 KW agonist; antagonist; vector; CHO; Chinese hamster ovary;  
 KW cell culture.

XX Homo sapiens.

XX WO9423038-A.

PN 13-OCT-1994.

XX 25-MAR-1994; 94WO-GB00621.

XX 26-MAR-1993; 93GB-0006386.

XX (WELL ) WELLCOME FOUND LTD.

XX Charles IG, Moncada SE, Palmer RMJ, Moncada S;

XX WPI; 1994-333198/41.

XX N-PSDB; AAQ77700.

XX New human inducible nitric oxide synthase - useful for  
 PT identifying enzyme inhibitors and stimulators, and for diagnosis  
 PT and treatment of e.g. viral infections or tumours

PS Disclosure; Page 25-31; 42pp; English.

XX Human chondrocytes were incubated with interleukin-1-beta to induce  
 CC nitric-oxide-synthase. cDNA was generated and used to construct a  
 CC library in lambda ZAPII. This was screened with a 650 bp fragment of  
 CC mouse inducible NO-synthase cDNA to identify the full-length clone  
 CC pBSHSINOS. The insert was transferred to pSVL to give a vector  
 CC capable of expressing NO-synthase in CHO cells under control of a  
 CC heterologous constitutive promoter.

XX Sequence 1153 AA;

Query Match 100.0%; Score 95; DB 15; Length 1153;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVQGILERVVDGTPH 18  
 DB 781 palvqgilervvvdgtpgh 798

## RESULT 11

AA88464  
 ID AAR88464 standard; Protein; 1153 AA.

XX AAR88464;

DT 13-MAY-1996 (first entry)

DE Hepatocyte inducible nitric oxide synthase.

XX Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy;  
 KW vascular occlusive disease; cancer; infection.

XX Homo sapiens.

PN WO9600006-A1.

XX 04-JAN-1996.

PF 20-JUN-1995; 95WO-US07849.

PR 24-JUN-1994; 94US-025046.

XX (UVP1-) UNIV PITTSBURGH.

PI Billiar TR, Geller DA, Nussler AK, Simmons RL, Tzeng E;

DR WPI; 1996-068641/07.

DR N-PSDB; AAT10115.

XX Inducible nitric oxide synthase gene - useful in gene therapy to  
 PT treat, e.g. vascular occlusive disease and cancer

PS Disclosure; Page 54-58; 91pp; English.

XX An inducible nitric oxide synthase (iNOS = AAR88464) is the product  
 CC of a cDNA clone (AAT10115) derived from human hepatocytes induced  
 CC for iNOS biosynthesis. The iNOS can be obtd. by expression of  
 CC the cDNA e.g. in mammalian host cells and is used in the  
 CC development of selective inhibitors of NOS or to treat diseases  
 CC affected by nitric oxide.

XX Sequence 1153 AA;

Query Match 100.0%; Score 95; DB 17; Length 1153;

Best Local Similarity 100.0%; Pred. No. 8.4e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVQGILERVVDGTPH 18

DB 781 palvqgilervvvdgtpgh 798

## RESULT 12

AAW36113  
 ID AAW36113 standard; Protein; 1153 AA.

XX AAW36113;

DT 11-MAY-1998 (first entry)

DE Human inducible nitric oxide synthetase.

XX Nitric oxide synthetase; NOS; iNOS; HPiNOS; human;

KW erectile dysfunction; impotence; gene therapy; corpora cavernosa;  
 KW relaxant.

XX

OS Homo sapiens.  
 XX WO9742965-A1.  
 PN 20-NOV-1997.  
 PD 09-MAY-1997; 97WO-US07643.  
 PF 10-MAY-1996; 96US-0017373.  
 PR (GONZ/) GONZALEZ-CADAVID N F.  
 XX (RAJF/) RAJFER J.  
 PA Gonzalez-Cadavid NF, Rajfer J;  
 PI WPI; 1998-008577/01.  
 DR N-PSDB; AAT98199.

XX Treatment of erectile dysfunction - by introducing an agent into  
 PT penile tissue, particularly for inducing cavernosal smooth muscle  
 PT relaxation or increasing NOS levels

XX Claim 12; Page 38-41; 53pp; English.

XX This protein comprises human penis inducible nitric oxide  
 CC synthetase (HPiNOS). Its amino acid sequence was deduced from a  
 CC cDNA clone (See AAT98199) derived from human penile smooth muscle  
 CC cell mRNA. The invention is directed to a method of treating  
 CC erectile dysfunction in a patient by providing an agent capable of  
 CC treating erectile dysfunction, and introducing an effective amount  
 CC of the agent into the penile tissue of the patient. Preferably,  
 CC the agent induces cavernosal smooth muscle relaxation, and/or  
 CC produces an increase in the level of NOS in tissue. Preferably,  
 CC the NOS is iNOS, and the agent is introduced into the corpora  
 CC cavernosa of the penis. The agent is preferably an NOS inducer, an  
 CC NOS protein such as HPiNOS, a cDNA encoding an NOS such as HPiNOS,  
 CC or cDNA transformed penile cells, especially corpora cavernosa  
 CC cells.

XX Sequence 1153 AA;

Query Match 100.0%; Score 95; DB 19; Length 1153;

Best Local Similarity 100.0%; Pred. No. 8.4e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVQGILERVVDGTPH 18

DB 781 palvqgilervvvdgtpgh 798

## RESULT 13

AAB31724

ID AAB31724 standard; Protein; 1153 AA.

XX AAB31724;

AC 30-APR-2001 (first entry)

XX Amino acid sequence of a human inducible nitric oxide synthase (NOS).  
 DE Gene therapy; angiogenesis; nucleic acid delivery; arteriosclerosis;  
 KW nitric oxide synthase; NOS; endothelial dysfunction.

XX Homo sapiens.

PN WO200103728-A2.

XX 18-JAN-2001.

XX 07-JUL-2000; 2000WO-NL00482.

XX 09-JUL-1999; 99EP-0202263.



PR 09-JUL-1999; 99US-0143101.  
 XX (INTR-) INTROGENE BV.  
 XX Vogels R, Verlinden SFF;  
 XX WPI; 2001-123142/13.  
 XX Nucleic acid delivery vehicle comprising a nucleic acid encoding nitric  
 PT oxide synthase, used for isolated tissue perfusion treatment to enhance  
 PT and induce angiogenesis -  
 XX  
 PS Disclosure; Fig 6; 37pp; English.  
 XX  
 CC The specification describes a method for gene therapy for enhancing  
 CC and inducing angiogenesis. The method uses a nucleic acid delivery  
 CC vehicle, which comprises a nucleic acid encoding nitric oxide synthase  
 CC (NOS). The delivery vehicle is used for the manufacture of a  
 CC pharmaceutical composition for isolated tissue perfusion treatment.  
 CC The method is useful for enhancing and/or inducing angiogenesis in  
 CC patients with endothelial dysfunctions, in particular arteriosclerosis.  
 CC The present sequence represents an inducible NOS.  
 XX  
 SQ Sequence 1153 AA;

Query Match 100.0%; Score 95; DB 22; Length 1153;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVQIGILERVVDGPTPH 18  
 .|||||  
 Db 781 palvqgillervvdgptph 798

RESULT 14  
 AAB66724  
 ID AAB66724 standard; protein; 1153 AA.  
 XX  
 AC AAB66724;  
 XX  
 DT 09-APR-2001 (first entry)  
 XX  
 DE Human inducible nitric oxide synthase.  
 XX  
 KW Nitric oxide synthase; NOS; angiogenesis; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1067190-A1.  
 XX  
 PD 10-JAN-2001.  
 XX  
 PF 09-JUL-1999; 99EP-0202263.  
 XX  
 PR 09-JUL-1999; 99EP-0202263.  
 XX  
 PA (INTR-) INTROGENE BV.  
 XX  
 PI Vogels R, Verlinden S;  
 XX  
 DR WPI; 2001-125729/14.  
 XX  
 XX Use of a nucleic acid delivery vehicle comprising a nucleic acid  
 PT encoding nitric oxide synthase, especially useful in gene therapy for  
 PT enhancing and/or inducing angiogenesis and treating atherosclerosis -  
 XX  
 PS Examples; Page 14-18; 39pp; English.  
 XX  
 CC The present invention relates to use of a nucleic acid delivery  
 CC vehicle comprising a nucleic acid encoding nitric oxide synthase  
 CC (NOS) activity for the manufacture of a composition for essentially  
 CC isolated tissue perfusion treatment to enhance and/or induce

CC angiogenesis. The nucleic acid delivery vehicle is particularly  
 CC useful in gene therapy for the treatment of atherosclerosis.  
 XX  
 SQ Sequence 1153 AA;

Query Match 100.0%; Score 95; DB 22; Length 1153;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALVQIGILERVVDGPTPH 18  
 .|||||  
 Db 781 palvqgillervvdgptph 798

RESULT 15  
 AAW81233  
 ID AAW81233 standard; peptide; 15 AA.  
 XX  
 AC AAW81233;  
 XX  
 DT 30-APR-1999 (first entry)  
 XX  
 DE Human INOS peptide fragment PS-5222.  
 XX  
 KW Inducible; nitric oxide synthase; INOS; human; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
 KW autoimmune disease; multiple sclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 15  
 FT /note= "His residue amidated"  
 XX  
 PN WO9845710-A1.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PF 11-APR-1997; 97WO-US06500.  
 XX  
 PR 07-APR-1997; 97US-666777.  
 XX  
 PA (WEBB/) WEBBER R.  
 XX  
 PI Webber R;  
 XX  
 DR WPI; 1998-594495/50.  
 XX  
 PT Detection of human inducible nitric oxide synthase - using an  
 PT immunoassay in which a sample is contacted with a specific binding  
 PT entity reactive with human INOS or mimics.  
 XX  
 PS Example 4; Page 36; 93pp; English.  
 XX  
 CC This invention describes an immunoassay method where a sample with a  
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
 CC inducible nitric oxide synthase (INOS) or mimics of this protein is used  
 CC to detect the presence of human INOS protein in the sample. The method  
 CC can be used for the detection and quantitation of human INOS in cells and  
 CC tissues for various pathological conditions such as sepsis, septic  
 CC shock, myocardial infarction, rejection of tissue in organs following  
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
 CC represents a peptide from human INOS which is used in the method of the  
 CC invention.  
 XX  
 SQ Sequence 15 AA;

Query Match 84.2%; Score 80; DB 19; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;

Matches	15;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	4	VQGIILERVVDGPTPH	18						
Db	1	vqgillervvdgptph	15						

Search completed: September 10, 2001, 14:00:25  
Job time: 169 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:11:13 ; Search time 72.54 Seconds  
(without alignments)  
32.830 Million cell updates/sec

Title: US-08-833-506c-31  
Perfect score: 97  
Sequence: 1 RMTLVFGSRPPDEHHYQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL16: \*  
2: sp\_archaea: \*  
3: sp\_bacteria: \*  
4: sp\_fungi: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organellae: \*  
9: sp\_phage: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_unclassified: \*  
13: sp\_vertebrate: \*  
14: sp\_virus: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	92	94.8	1114	4	O94994 homo sapien
2	86	88.7	1154	6	O97604 canis famil
3	81	83.5	945	6	O9N175 ovis aries
4	81	83.5	1147	11	O9ROW4 rattus norv
5	74	76.3	82	6	O9TTT6 oryctolagus
6	68	70.1	1147	11	O9QW28 rattus sp.
7	56	57.7	1127	13	O9F092 cyprinus ca
8	52	53.6	662	5	O9Q590 caenorhabdi
9	52	53.6	687	5	O9NKV3 bombyx mori
10	51	52.6	306	11	O9JJY7 rattus norv
11	51	52.6	366	6	O9N176 ovis aries
12	51	52.6	1205	6	O9TUX8 canis famil
13	51	52.6	1206	11	O9WTK6 Q9WTK6 cavia porce
14	49	50.5	667	11	O60451 cricetus
15	49	50.5	677	4	O9H3M8 homo sapien
16	48	49.5	614	5	O15702 dictyosteli
17	46	47.4	693	3	O00141 aspergillus
18	45	46.4	366	5	O16550 caenorhabdi
19	45	46.4	623	3	Q12181 saccharomyc

20	45	46.4	701	5	P91655
21	44	45.4	278	2	O9F4D7
22	44	45.4	340	5	O9VP28
23	44	45.4	629	3	O9P4E1
24	44	45.4	1342	5	O9GPP6
25	43	44.3	201	5	O9NA92
26	43	44.3	211	2	O46063
27	43	44.3	690	3	O9HG14
28	43	44.3	736	3	O9HDG2
29	42	43.3	240	10	O9LDW2
30	42	43.3	244	2	O9KB53
31	42	43.3	330	1	O9YCT1
32	42	43.3	390	5	O9XYU9
33	42	43.3	433	5	O18479
34	42	43.3	444	4	O9NXJ6
35	42	43.3	539	4	O9HCC8
36	41	42.3	161	2	O9RZ18
37	41	42.3	311	1	O9HNX6
38	41	42.3	413	10	O9LXS0
39	41	42.3	422	2	O9X8X3
40	41	42.3	531	10	O9FP93
41	41	42.3	698	4	O60471
42	41	42.3	725	4	O9UBK8
43	41	42.3	1091	5	O9W126
44	41	42.3	3290	10	O9SH73
45	40.5	41.8	632	1	O9UY08

## ALIGNMENTS

RESULT 1

O94994 ID O94994 PRELIMINARY; PRT: 1114 AA.  
AC O94994;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE INDUCIBLE NITRIC OXIDE SYNTHASE.  
GN INOS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_Taxid-9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ogawa Y., Nishijima S., Goto M., Ida M.;  
RT "Cloning and characterization of a novel splice variant of human  
RT inducible nitric oxide synthase.";  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB022318; BAA37123.1; -;  
DR HSSP; P35228; 4NOS.  
DR InterPro; IPR001094; -;  
DR InterPro; IPR001433; -;  
DR InterPro; IPR003097; -;  
DR Pfam; PF00175; oxidored\_fad; 1.  
DR Pfam; PF00667; FAD\_binding; 1.  
DR PRINTS; PR00369; FLAVODOXIN.  
DR PRINTS; PR00371; FPNCR.  
SQ SEQUENCE 1114 AA; 126748 MW; C1F9624774435571 CRC64;

Query Match 94.8%; Score 92; DB 4; Length 1114;  
Best Local Similarity 94.4%; Pred. No. 4.2e-07;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RMTLVFGSRPPDEHHYQ 18

Db 970 RMTLVFGSRPPDEHHYQ 987

RESULT 2

DR	ENBL; AF223942; AAF34710.1; -.	
DR	InterPro; IPR001094; -	
DR	InterPro; IPR001433; -	
DR	InterPro; IPR001709; -	
DR	InterPro; IPR003097; -	
DR	Pfam; PF00175; oxidored_fad; 1.	
DR	Pfam; PF00667; FAD_binding; 1.	
DR	PRINTS; PR00369; FLAVODOXIN.	
DR	PRINTS; PR00371; FENCR.	
FT	NON_TER	1
FT	TER	945
SQ	SEQUENCE	945 AA; 108001 MW; 9A5ACFD04040A74F CRC64;

Query Match 83.5%; Score 81; DB 11; Length 1147;  
Best Local Similarity 77.8%; Pred. No. 3.2e-05;  
Matches 14; Conservative 2; Mismatches 2; Indels

```

QY 1 RMTLVFSGRRPDEDHIYQ 18
  ||||| | | | | | | | |
Db 1006 RMTLVFSGRRPDEDHIYQ 1023

RESULT 5
Q9TTT6 PRELIMINARY; PRT; 82 AA.
AC Q9TTT6;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TEMBLrel. 16, Last annotation update)
DE INDUCIBLE NITRIC OXIDE SYNTHASE NOS2 (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE; TISSUE-KIDNEY;
RA Tsao L.S., O'Brien W.J.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE; TISSUE-HEART MYOCARDIUM;
RX PubMed=11053770;
RA Shi Y., Pritchard K.A., Baker J.E.;
RT "Chronic myocardial hypoxia increases nitric oxide synthase and
  decreases caveolin-3.";
RL Free Radic. Biol. Med. 29:695-703(2000).
DR EMBL; AF198443; AAF09500.1; -.
DR EMBL; AF200351; AAG24286.1; -.
DR HSSP; P00388; 1AMO.
DR InterPro; IPR001709; -.
DR PRINTS; PR00371; FPNCR.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9396 MW; 73244479A4B965F6 CRC64;

Query Match 76.3%; Score 74; DB 6; Length 82;
Best Local Similarity 76.5%; Pred. No. 3e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RMTLVFSGRRPDEDHIY 17
  ||||| | | | | |
Db 55 RMTLVFSGRRPDEDHIY 71

RESULT 6
Q9QW28 PRELIMINARY; PRT; 1147 AA.
AC Q9QW28;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE CYTOKINE INDUCIBLE NITRIC OXIDE SYNTHASE, INOS.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=93221515; PubMed=7682072;
RA Wood E.R., Berger H.Jr., Sherman P.A., Lapetina E.G.;
RT "Hepatocytes and macrophages express an identical cytokine inducible
  nitric oxide synthase gene.";
RL Biochem. Biophys. Res. Commun. 191:767-774(1993).
DR HSSP; P29477; 1NOS.
DR InterPro; IPR001094; -.
DR InterPro; IPR001433; -.
DR InterPro; IPR001709; -.
DR InterPro; IPR002369; -.

Query Match 57.7%; Score 56; DB 13; Length 1127;
Best Local Similarity 58.8%; Pred. No. 0.58;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 MTLVFGSRPDEDHIYQ 18
  :||| | | | | |
Db 1007 VTLVFGSGRSDTHLYK 1023

RESULT 8
Q09590 PRELIMINARY; PRT; 662 AA.
AC Q09590;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)

```

```

DR InterPro; IPR003097; -.
DR Pfam; PF00175; oxidored_fad; 1.
DR PRINTS; PR00667; FAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR ProDom; PD001811; -.
SQ SEQUENCE 1147 AA; 130625 MW; 2CAFB983E56F651A CRC64;

Query Match 70.1%; Score 68; DB 11; Length 1147;
Best Local Similarity 72.2%; Pred. No. 0.0053;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RMTLVFSGRRPDEDHIYQ 18
  ||||| | | | | |
Db 1006 RMTLVFSGRRPDEDHIYQ 1023

RESULT 7
Q9PU92 PRELIMINARY; PRT; 1127 AA.
AC Q9PU92;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE INDUCIBLE NITRIC OXIDE SYNTHASE (EC 1.14.13.39).
GN INOS.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
[1]
RN SEQUENCE FROM N.A.
RA Saeij J.P., Stet R.J., Groeneveld A., Verborg-van Kemenade L.B.,
RT "Identification and characterization of a fish inducible nitric oxide
  synthase cDNA.";
RL Immunogenetics 0:0-0(0).
DR EMBL; AJ242906; CAB60197.1; -.
DR HSSP; P29477; 1NOS.
DR InterPro; IPR001094; -.
DR InterPro; IPR001433; -.
DR InterPro; IPR001522; -.
DR InterPro; IPR001709; -.
DR InterPro; IPR002106; -.
DR InterPro; IPR003097; -.
DR Pfam; PF00175; oxidored_fad; 1.
DR PRINTS; PR00667; FAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR ProDom; PD002221; -.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 1127 AA; 127431 MW; 8317FC67C7A3DD9A CRC64;

Query Match 57.7%; Score 56; DB 13; Length 1127;
Best Local Similarity 58.8%; Pred. No. 0.58;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 MTLVFGSRPDEDHIYQ 18
  :||| | | | | |
Db 1007 VTLVFGSGRSDTHLYK 1023

RESULT 8
Q09590 PRELIMINARY; PRT; 662 AA.
AC Q09590;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)

```



```

GN 23B.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Mershon J.L., Clark K.E.;
RT "Estrogen increases the expression of iNOS in the ovine coronary
RT artery.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF223471; AAF34707.1; -.
DR InterPro: IPR001433; -.
DR InterPro: IPR001709; -.
DR InterPro: IPR003097; -.
DR Pfam: PF00175; oxidored_fad; 1.
DR Pfam: PF00667; FAD_binding; 1.
DR PRINTS: PR00371; FPNCR.
FT NON_TER 1
FT NON_TER 366
FT SEQUENCE 366 AA; 40791 MW; 794B274DA7864A0 CRC64;

Query Match 52.6%; Score 51; DB 6; Length 366;
Best Local Similarity 58.8%; Pred. No. 1.2;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTLVFGSRRPDEHHYQ 18
||||| I ||:|
Db 289 MTLVFGCRCSQLDHLYR 305

RESULT 12
Q9TUX8 PRELIMINARY; PRT; 1205 AA.
AC Q9TUX8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE NITRIC OXIDE SYNTHASE.
GN NOS.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX MEDLINE=99369487; PubMed=10442857;
RA Schwemmer M., Bassenge E.;
RT "Assembly and characterization of canine heart endothelial nitric
RT oxide synthase cDNA and 5'-flanking sequence by homology (RT)-PCR
RT cloning.";
RL Nitric Oxide 3:254-264(1999).
DR EMBL: AF143503; AAD52161.1; -.
DR HSSP: P29474; 3NOS.
DR InterPro: IPR001094; -.
DR InterPro: IPR001433; -.
DR InterPro: IPR001709; -.
DR InterPro: IPR003097; -.
DR Pfam: PF00175; oxidored_fad; 1.
DR Pfam: PF00667; FAD_binding; 1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
SQ SEQUENCE 1205 AA; 133045 MW; C150CDEB01685BA5 CRC64;

Query Match 52.6%; Score 51; DB 6; Length 1205;
Best Local Similarity 58.8%; Pred. No. 4.4;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTLVFGSRRPDEHHYQ 18
||||| I ||:|

```

```

Db 1044 MTLVFGCRCSQLDHLYR 1060
||||| I ||:|

RESULT 13
Q9WTK6 PRELIMINARY; PRT; 1206 AA.
AC Q9WTK6;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ENDOTHELIAL NITRIC OXIDE SYNTHASE.
GN NOS3.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Derst C., Preisig-Mueller R., Rajan S., Daut J.;
RT "Cloning and sequencing of guinea pig NO synthases.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF146041; AAD29753.1; -.
DR EMBL: AF146040; AAD29752.1; -.
DR HSSP: P29474; 3NOS.
DR InterPro: IPR001094; -.
DR InterPro: IPR001433; -.
DR InterPro: IPR001709; -.
DR InterPro: IPR003097; -.
DR Pfam: PF00175; oxidored_fad; 1.
DR Pfam: PF00667; FAD_binding; 1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
SQ SEQUENCE 1206 AA; 133692 MW; EB4E792D3F9503DD CRC64;

Query Match 52.6%; Score 51; DB 11; Length 1206;
Best Local Similarity 58.8%; Pred. No. 4.4;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTLVFGSRRPDEHHYQ 18
||||| I ||:|
Db 1045 MTLVFGCRCSQLDHLYR 1061

RESULT 14
Q60451 PRELIMINARY; PRT; 667 AA.
AC Q60451;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE NADPH-CYTOCHROME P450 OXIDOREDUCTASE.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GOLDEN;
RA Ohguya S., Goda T., Hoshino T., Shinriki N., Kamataki T.;
RT "High-red yeast, construction of a novel strain of Saccharomyces
RT cerevisiae stably exerting high activity of hamster cytochrome P450
RT reductase.";
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: D83230; BAA11856.1; -.
DR HSSP: P00388; IAWO.
DR InterPro: IPR001094; -.
DR InterPro: IPR001433; -.
DR InterPro: IPR001709; -.
DR InterPro: IPR003097; -.
DR Pfam: PF00175; oxidored_fad; 1.

```

DR Pfam; PF00667; FAD\_binding; 1.  
DR PRINTS; PR00369; FLAVODOXIN.  
DR PRINTS; PR00371; FPNCR.  
KW NADP.  
SQ SEQUENCE 667 AA; 75850 MW; 2023F43DF4C1EF07 CRC64;

Query Match 50.5%; Score 49; DB 11; Length 667;  
Best Local Similarity 53.3%; Pred. No. 5.2;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LVFGSRRPDEHIYQ 18  
| : | | | | : : |  
Db 551 LVYGCRSDEYLYR 565

## RESULT 15

Q9H3M8  
ID Q9H3M8 PRELIMINARY; PRT; 677 AA.  
AC Q9H3M8;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE NADPH-CYTOCHROME P-450 REDUCTASE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Murakami H.O., Ogawa H., Nisimoto Y.;  
RT "cDNA cloning and characterization of NADPH-cytochrome P-450 reductase  
in human HL-60 cell.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB051763; BAB18572.1; -.  
SQ SEQUENCE 677 AA; 76637 MW; 4B414DCC3F1A3590 CRC64;

Query Match 50.5%; Score 49; DB 4; Length 677;  
Best Local Similarity 53.3%; Pred. No. 5.2;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LVFGSRRPDEHIYQ 18  
| : | | | | : : |  
Db 562 LVYGCRSDEYLYR 576

Search completed: September 10, 2001, 14:11:14  
Job time: 593 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:09:53 ; Search time 23.82 Seconds  
(without alignments)  
25.886 Million cell updates/sec

Title: US-08-833-506C-31

Perfect score: 97

Sequence: 1 RMTLVGSRPRDEDHVQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	92	94.8	1153	1	NS2A_HUMAN	P35228 homo sapien
2	81	83.5	246	1	NOS2_BOVIN	Q27995 bos taurus
3	81	83.5	496	1	NOS2_RABIT	O19114 oryctolagus
4	81	83.5	1147	1	NOS2_RAT	O6518 rattus norv
5	81	83.5	1147	1	NS2D_HUMAN	O60591 homo sapien
6	77	79.4	1144	1	NOS2_MOUSE	P29477 mus musculus
7	76	78.4	1149	1	NOS2_CAVPO	O54705 cavia porce
8	66	68.0	79	1	NS2B_HUMAN	P81272 homo sapien
9	62	63.9	1136	1	NOS2_CHICK	Q90703 gallus gall
10	59	60.8	1136	1	NS2C_HUMAN	Q14961 homo sapien
11	52	53.6	1054	1	CYPE_BACSU	O08336 bacillus su
12	51	52.6	919	1	NOS3_RAT	Q62600 rattus norv
13	51	52.6	1048	1	CPXB_BACME	P14779 bacillus me
14	51	52.6	1201	1	NOS3_MOUSE	P70313 mus musculus
15	51	52.6	1201	1	NOS3_HUMAN	P29474 homo sapien
16	51	52.6	1204	1	NOS3_BOVIN	P29474 homo sapien
17	51	52.6	1204	1	NOS1_MOUSE	Q92069 sus scrofa
18	51	52.6	1429	1	NOS1_PIG	Q92069 sus scrofa
19	51	52.6	1429	1	NOS1_RAT	P29476 rattus norv
20	51	52.6	1434	1	NOS1_HUMAN	P29476 homo sapien
21	51	52.6	1435	1	NOS1_RABIT	O19132 oryctolagus
22	49	50.5	676	1	NCPR_HUMAN	P16435 homo sapien
23	49	50.5	677	1	NCPR_CAVPO	P37039 cavia porce
24	49	50.5	677	1	NCPR_MOUSE	P37040 mus musculus
25	49	50.5	677	1	NCPR_PIG	P04175 sus scrofa
26	49	50.5	677	1	NCPR_RAT	P00388 rattus norv
27	48	49.5	671	1	NCPR_MUSDO	Q07994 musca domes
28	45	46.4	16	1	PPAC_BACME	P36948 bacillus me
29	45	46.4	679	1	NCPR_DROME	Q27597 drosophila
30	43	44.3	1146	1	MFD_HAEIN	P45128 haemophilus
31	42	43.3	424	1	CUT1_CAEEL	O03755 caenorhabdi
32	41	42.3	305	1	R1R2_HSVSA	O01038 herpesvirus
33	41	42.3	310	1	PPAC_STRMU	O68579 streptococc

#### RESULT 1

ID	NS2A_HUMAN	STANDARD;	PRT;	1153 AA.
AC	P35228; Q16692; O60757; Q16263;			
DC	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)			
DE	(INDUCIBLE NOS) (INOS) (HEPATOCYTE NOS) (HEP-NOS).			
GN	NOS2A OR NOS2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RX	SEQUENCE FROM N.A.			
RP	TISSUE=Liver;			
RC	TISSUE=Chondrocytes;			
RX	MEDLINE=932334523; PubMed=7682706;			
RA	Geller D.A., Lowenstein C.J., Shapiro R.A., Nussler A.K.,			
RA	di Silvio M., Wang S.C., Nakayama D.K., Simmons R.L., Snyder S.H.,			
RA	Billiar T.R.;			
RT	"Molecular cloning and expression of inducible nitric oxide synthase			
RT	from human hepatocytes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:3491-3495(1993).			
RN	[2]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Colorectal adenocarcinoma;			
RA	MEDLINE=94032282; PubMed=7692964;			
RA	Sherman P.A., Laubach V.E., Reep B.R., Wood E.R.;			
RT	"Purification and cDNA sequence of an inducible nitric oxide synthase			
RT	from a human tumor cell line.";			
RL	Biochemistry 32:11600-11605(1993).			
RN	[3]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Chondrocytes;			
RX	MEDLINE=94068614; PubMed=7504305;			
RA	Charles I.G., Palmer R.M.J., Hickery M.S., Bayliss M.T.,			
RA	Chubb A.P., Hall V.S., Moss D.W., Moncada S.;			
RT	"Cloning, characterization, and expression of a cDNA encoding an			
RT	inducible nitric oxide synthase from the human chondrocyte.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:11419-11423(1993).			
RN	[4]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Articular chondrocytes;			
RX	MEDLINE=94368816; PubMed=7522054;			
RA	Maier R., Bilbe G., Rediske J., Lotz M.;			
RT	"Inducible nitric oxide synthase from human articular chondrocytes:			
RT	cDNA cloning and analysis of mRNA expression.";			
RL	Biochim. Biophys. Acta 1208:145-150(1994).			
RN	[5]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Retina;			
RX	MEDLINE=95091827; PubMed=7528017;			
RA	Park C.S., Pardhasaradhi K., Gianotti C., Villegas E., Krishna G.;			
RT	"Human retina expresses both constitutive and inducible isoforms of			
RT	nitric oxide synthase mRNA.";			

#### ALIGNMENTS

34	41	42.3	311	1	PPAC_STRGC	P95765 streptococc
35	41	42.3	679	1	NCPR_RABIT	P00389 oryctolagus
36	40	41.2	274	1	NHS_STRAS	P52391 streptomyce
37	40	41.2	522	1	CYSJ_THIRO	P52674 thiocapsa r
38	40	41.2	1074	1	ACA8_ARATH	Q91679 arabidopsis
39	40	41.2	4655	1	LRP2_HUMAN	P98164 homo sapien
40	39	40.2	309	1	PPAC_BACSU	P37487 bacillus su
41	39	40.2	336	1	G3PC_PETCR	P25519 petroselinu
42	39	40.2	349	1	F16P_RHIME	P56886 rhizobium m
43	39	40.2	483	1	NIFE_METMP	P71528 methanococc
44	39	40.2	586	1	AYM_BACAD	P32818 bacillus ac
45	39	40.2	601	1	NCPR_SALTR	P19618 salmo trutt

RL Biochem. Biophys. Res. Commun. 205:85-91(1994).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Glioblastoma;  
 RX MEDLINE=95155267; PubMed=7531687;  
 RA Hokari A., Zeniya M., Esumi H.;  
 RT "Cloning and functional expression of human inducible nitric oxide  
 synthase (NOS) cDNA from a glioblastoma cell line A-172.";  
 RL J. Biochem. 116:575-581(1994).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Airway epithelium;  
 RX MEDLINE=95372368; PubMed=7544004;  
 RA Guo F.H., de Raevae R.H., Rice T.W., Stuehr D.J., Thunnissen F.B.J.M.,  
 ERzurum S.C.;  
 RT "Continuous nitric oxide synthesis by inducible nitric oxide synthase  
 in normal human airway epithelium in vivo.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7809-7813(1995).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cardiac myocytes;  
 RX MEDLINE=97304504; PubMed=9160867;  
 RA Lues H., Li R.-K., Shapiro R.A., Tzeng E., McGowan F.X., Yoneyama T.,  
 RA Hatakayama K., Geller D.A., Mickie D.A.G., Simmons R.L.,  
 RA Billiar T.R.;  
 RT "Differentiated human ventricular cardiac myocytes express  
 inducible nitric oxide synthase mRNA but not protein in response to  
 IL-1, TNF, IFN-gamma, and LPS.";  
 RL J. Mol. Cell. Cardiol. 29:1153-1165(1997).  
 RN [9]  
 RP SEQUENCE OF 380-473 FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=95165725; PubMed=7532248;  
 RA McLaughlin J.S., Chatterjee P., Nicolson A.G., Jardine A.G., McKay N.G.,  
 RA Ralston S.H., Grabow P., Haitsen N.E., Macleod A.M.,  
 RA Hawksworth G.M.;  
 RT "Nitric oxide production by human proximal tubular cells: a novel  
 immunomodulatory mechanism?";  
 RL Kidney Int. 46:1043-1049(1994).  
 RN [10]  
 RP CHARACTERIZATION.  
 RX MEDLINE=96047340; PubMed=7558036;  
 RA Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G.,  
 RA Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;  
 RT "Three members of the nitric oxide synthase II gene family (NOS2A,  
 NOS2B, and NOS2C) colocalize to human chromosome 17.";  
 RL Genomics 27:526-530(1995).  
 RN [11]  
 RP CHARACTERIZATION.  
 RX MEDLINE=98389865; PubMed=9721329;  
 RA Taylor B.S., Alarcon L.H., Billiar T.R.;  
 RT "Inducible nitric oxide synthase in the liver: regulation and  
 function.";  
 RL Biochimica 63:766-781(1998).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 74-504.  
 RX MEDLINE=99340067; PubMed=10409685;  
 RA Li H., Raman C.S., Glaser C.B., Blasko E., Young T.A., Parkinson J.F.,  
 RA Whitlow M., Poulos T.L.;  
 RT "Crystal structures of zinc-free and -bound heme domain of human  
 inducible nitric-oxide synthase. Implications for dimer stability and  
 comparison with endothelial nitric-oxide synthase.";  
 RL J. Biol. Chem. 274:21276-21284(1999).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 82-528.  
 RX MEDLINE=99173237; PubMed=10074942;  
 RA Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,  
 RA Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,  
 RA Weber P.C.;  
 RT "Structural characterization of nitric oxide synthase isoforms  
 reveals striking active-site conservation.";  
 RL Nat. Struct. Biol. 6:233-242(1999).  
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE

CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO  
 CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.  
 CC -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +  
 CC NITRIC OXIDE + N NADP(+).  
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 CC TETRAHYDROBIPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 CC THE ENZYME (BY SIMILARITY).  
 CC -1- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST  
 CC WITH MOUSE NOS2). ASPIRIN INHIBITS EXPRESSION AND FUNCTION OF THIS  
 CC ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF  
 CC TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE  
 CC CATALYTIC ACTIVITY (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE LIVER, RETINA, BONE CELLS AND  
 CC AIRWAY EPITHELIAL CELLS OF THE LUNG. NOT EXPRESSED IN THE  
 CC PLATELETS.  
 CC -1- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES.  
 CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; L09210; AAA59171.1; -;  
 CC EMBL; L24553; AAA36375.1; -;  
 CC EMBL; X73029; CAA51512.1; -;  
 CC EMBL; U05810; AAA56666.1; -;  
 CC EMBL; U31511; AAB49041.1; -;  
 CC EMBL; D26525; BAA05531.1; -;  
 CC EMBL; U20141; AAB60366.1; -;  
 CC EMBL; AF068236; AAC19133.1; -;  
 CC EMBL; S75615; AAD14179.1; -;  
 CC PIR; A47475; A47475.  
 CC PDB; 1NSI; 07-JAN-00.  
 CC PDB; 2NSI; 07-JAN-00.  
 CC PDB; 4NOS; 04-FEB-00.  
 CC MIN; I63730; -;  
 CC InterPro; IPR001094; -;  
 CC InterPro; IPR001433; -;  
 CC InterPro; IPR001709; -;  
 CC InterPro; IPR003097; -;  
 CC Pfam; PF00667; FAD\_binding; 1.  
 CC Pfam; PF00175; oxidored\_fad; 1.  
 CC PRINTS; PR00369; FLAVODOXIN.  
 CC PRINTS; PR00371; FPNCR.  
 CC Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;  
 CC Heme; Phosphorylation; Zinc; Metal-binding; Multigene family;  
 CC 3D-structure.  
 CC BINDING 200 200  
 CC DOMAIN 509 529  
 CC NP\_BIND 623 654  
 CC NP\_BIND 767 778  
 CC NP\_BIND 903 913  
 CC NP\_BIND 978 996  
 CC NP\_BIND 1076 1091  
 CC METAL 110 110  
 CC METAL 115 115  
 CC MOD\_RES 234 234  
 CC MOD\_RES 578 578  
 CC MOD\_RES 892 892  
 CC CONFLICT 23 23  
 CC CONFLICT 154 154  
 CC CONFLICT 177 177  
 CC CONFLICT 266 266  
 CC CONFLICT 423 423  
 CC CONFLICT 439 439  
 CC CONFLICT 608 608  
 CC CONFLICT 676 676  
 CC CONFLICT 800 800  
 CC HEME.  
 CC CALMODULIN-BINDING (POTENTIAL).  
 CC FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 CC FAD (ADP PART) (BY SIMILARITY).  
 CC FAD (FLAVIN PART) (BY SIMILARITY).  
 CC NADP (RIBOSE PART) (BY SIMILARITY).  
 CC NADP (ADP PART) (BY SIMILARITY).  
 CC ZINC.  
 CC PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 CC PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 CC PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 CC D -> G (IN REF. 4).  
 CC F -> L (IN REF. 4).  
 CC G -> V (IN REF. 4).  
 CC R -> H (IN REF. 8).  
 CC L -> I (IN REF. 2).  
 CC A -> T (IN REF. 8).  
 CC S -> L (IN REF. 5 AND 6).  
 CC T -> I (IN REF. 7).  
 CC T -> A (IN REF. 4).

Query Match 94.8%; Score 92; DB 1; Length 1153;  
 Best Local Similarity 94.4%; Pred. NO. 9.2e-08;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RMTLVFGRRRPDEHHYQ 18  
 ||||| ||||| ||||| |||||

Db 1009 RMTLVFGRRRPDEHHYQ 1026

# RESULT 2

NOS2\_BOVIN  
 ID NOS2\_BOVIN STANDARD; PRT; 246 AA.  
 AC Q27995; Q27985;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)  
 DE (INDUCIBLE NOS) (INOS) (NOSII) (FRAGMENTS).  
 GN NOS2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;

[1]

SEQUENCE OF 1-110 FROM N.A.

RC TISSUE-Bone marrow macrophage;  
 RX MEDLINE=95238970; PubMed=7536776;  
 RA Adler H., Frech B., Thoeny M., Pfister H., Peterhans E., Jung T.W.,  
 RT "Inducible nitric oxide synthase in cattle. Differential cytokine  
 regulation of nitric oxide synthase in bovine and murine  
 macrophages";  
 RL J. Immunol. 154:4710-4718(1995).  
 RN [2]

SEQUENCE OF 111-246 FROM N.A.

RC TISSUE-Pulmonary artery;  
 RX MEDLINE=96047340; PubMed=7558036;  
 RA Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G.,  
 RA Lepore J.J., Philippov G., Thomas J.E., Jacob H.J., Bloch D.B.;  
 RT "Three members of the nitric oxide synthase II gene family (NOS2A,  
 NOS2B, and NOS2C) colocalize to human chromosome 17";  
 RL Genomics 27:526-530(1995).  
 CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO  
 MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.  
 CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +  
 NITRIC OXIDE + N NADP(+).  
 CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 TETRAHYDROBIPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 THE ENZYME (BY SIMILARITY).  
 CC -!- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY  
 SIMILARITY).  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; U14640; AAC48470.1; -

DR EMBL; U18331; AAC48479.1; -

DR HSSP; P29477; 3NOD.

DR InterPro; IPR001433; -

DR Pfam; PF00175; oxidored\_fad; 1.

KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;

Multigene family.

FT NON\_TER 1 35 HEME (BY SIMILARITY).

SEQUENCE 35 35

FT BINDING 35 35

SEQUENCE 35 35

FT BINDING 35 35

SEQUENCE 35 35

FT BINDING 35 35

SEQUENCE 35 35

FT BINDING 35 35

SEQUENCE 35 35

FT NP\_BIND 200 215 NADP (ADP PART) (BY SIMILARITY).  
 FT NON\_CONS 110 111  
 FT NON\_TER 246 246  
 SQ SEQUENCE 246 AA; 28748 MW; 87C2E330C86A27F4 CRC64;

Query Match 83.5%; Score 81; DB 1; Length 246;  
 Best Local Similarity 82.4%; Pred. NO. 1.3e-06;  
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RMTLVFGRRRPDEHHY 17  
 ||||| ||||| ||||| |||||

Db 133 RMTLVFGRRRPDEHHY 149

# RESULT 3

NOS2\_RABIT  
 ID NOS2\_RABIT STANDARD; PRT; 496 AA.  
 AC O19114;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)  
 DE (INDUCIBLE NOS) (INOS) (FRAGMENT).  
 GN NOS2.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN-NEW ZEALAND WHITE; TISSUE-Heart;

RA Broner C.W., Eledath F.M.;

RT "Rabbit inducible nitric oxide synthase gene-NOS II.";

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.

CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +  
 NITRIC OXIDE + N NADP(+).

CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 TETRAHYDROBIPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF

THE ENZYME (BY SIMILARITY).

CC -!- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY  
 SIMILARITY).

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; U85094; AAB65618.1; -

DR HSSP; P00388; IAMO.

DR InterPro; IPR001433; -

DR Pfam; PF00667; FAD-binding; 1.

DR Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;

Multigene family.

FT NON\_TER 1 25 FMN (PYRIMIDINE PART) (BY SIMILARITY).

FT NP\_BIND <1 25 FAD (ADP PART) (BY SIMILARITY).

FT NP\_BIND 138 149 FAD (FLAVIN PART) (BY SIMILARITY).

FT NP\_BIND 274 284 NADP (RIBOSE PART) (BY SIMILARITY).

FT NP\_BIND 349 367 NADP (ADP PART) (BY SIMILARITY).

FT NP\_BIND 447 462 NADP (ADP PART) (BY SIMILARITY).

FT NON\_TER 496 496

SEQUENCE 496 AA; 56397 MW; A0A1D303C57F0EEC CRC64;

Query Match 83.5%; Score 81; DB 1; Length 496;  
 Best Local Similarity 77.8%; Pred. No. 2.8e-06;  
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RMTLVFGSRPDEHIYQ 18  
 ||||| | | | | |  
 DB 380 RMTLVFGCRHPEDHLYQ 397

RESULT 4  
 NOS2\_RAT  
 ID NOS2\_RAT STANDARD; PRT: 1147 AA.  
 AC Q06518; P97774; Q35765; Q35766; Q64558; Q64005; Q63267;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)  
 DE (INDUCIBLE NOS) (INOS).  
 GN NOS2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Vascular smooth muscle;  
 RX MEDLINE-93191721; PubMed=7680561;  
 RA Nunokawa Y., Ishida N., Tanaka S.;  
 RT "Cloning of inducible nitric oxide synthase in rat vascular smooth  
 muscle cells.";  
 RL Biochem. Biophys. Res. Commun. 191:89-94(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-WISTAR; TISSUE-Pancreatic islets;  
 RX MEDLINE-95309542; PubMed=7540573;  
 RA Karlsten A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J.,  
 RA Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,  
 RA Mandrup-Poulsen T., Boel E., Nerup J.;  
 RT "Cloning and expression of cytokine-inducible nitric oxide synthase  
 cDNA from rat islets of Langerhans.";  
 RL Diabetes 44:753-758(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Astrocytes;  
 RX MEDLINE-94231594; PubMed=7513765;  
 RA Gatea E., Reis D.J., Feinstein D.L.;  
 RT "Cloning and expression of inducible nitric oxide synthase from rat  
 astrocytes.";  
 RL J. Neurosci. Res. 37:406-414(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE-Liver;  
 RX MEDLINE-94039059; PubMed=7693462;  
 RA Adachi H., Iida S., Oguchi S., Onshima H., Suzuki H., Nagasaki K.,  
 RA Kawasaki H., Sugimura T., Esumi H.;  
 RT "Molecular cloning of a cDNA encoding an inducible  
 calmodulin-dependent nitric-oxide synthase from rat liver and its  
 expression in COS 1 cells.";  
 RL Eur. J. Biochem. 217:37-43(1993).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Hepatocytes;  
 RX MEDLINE-93221515; PubMed=7682072;  
 RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;  
 RT "Hepatocytes and macrophages express an identical cytokine inducible  
 nitric oxide synthase gene.";  
 RL Biochem. Biophys. Res. Commun. 191:767-774(1993).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Aorta;  
 RX MEDLINE-94325351; PubMed=7519448;  
 RA Geng Y.J., Almquist M., Hansson G.K.;  
 RT "cDNA cloning and expression of inducible nitric oxide synthase from

rat vascular smooth muscle cells.";  
 RL Biochim. Biophys. Acta 1218:421-424(1994).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Kosuga K., Yui Y., Hattori R., Sase K., Elzawa H., Aoyama T.,  
 RA Inoue R., Sasayama S.;  
 RT "Cloning of an inducible nitric oxide synthase from rat  
 polymorphonuclear neutrophils.";  
 RL Endothelium 2:217-221(1994).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97070590; PubMed=8913516;  
 RA Tsutsumishita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,  
 RA Futaki S., Niwa M.;  
 RT "Sequence analysis of inducible nitric oxide synthase in rat kidney,  
 lung, and uterus.";  
 RL Biol. Pharm. Bull. 19:1374-1376(1996).  
 RN [9]  
 RP SEQUENCE OF 426-788 FROM N.A.  
 RC STRAIN-DAHL/RAPP SALT SENSITIVE STRAIN; TISSUE-Vascular smooth muscle;  
 RX MEDLINE-98195092; PubMed=9535415;  
 RA Chen P.Y., Gladish R.D., Sanders P.W.;  
 RT "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp  
 salt-sensitive rats.";  
 RL Hypertension 31:918-924(1998).  
 RN [10]  
 RP SEQUENCE OF 509-740 FROM N.A.  
 RC STRAIN-WISTAR; TISSUE-Renal glomerulus;  
 RA Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;  
 RT "Advances in the studies of NO synthesis regulation in mesangial  
 cells.";  
 RL Nephrologia 16:35-39(1996).  
 RN [11]  
 RP SEQUENCE OF 479-655 FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Renal glomerulus;  
 RX MEDLINE-94276509; PubMed=7516453;  
 RA Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montani D.,  
 RA Klahr S.;  
 RT "Location of an inducible nitric oxide synthase mRNA in the normal  
 kidney.";  
 RL Kidney Int. 45:998-1005(1994).  
 RN [12]  
 RP SEQUENCE OF 420-479 FROM N.A.  
 RC TISSUE-Myocardium;  
 RA Michel T., Balligand J.-L.;  
 RT "Isolation and characterization of INOS from rat cardiocytes.";  
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.  
 CC -1- CATALYTIC ACTIVITY: L-ARGININE + NADPH + M O(2) -> CITRULLINE +  
 NITRIC OXIDE + N NADP(+).  
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 TETRAHYDROBIPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 THE ENZYME.  
 CC -1- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN  
 INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE  
 EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL  
 MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY  
 SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY IN THE  
 MEDULLARY THICK ASCENDING LIMB, WITH MINOR AMOUNTS IN THE  
 MEDULLARY COLLECTING DUCT AND VASA RECTA BUNDLE.  
 CC -1- INDUCTION: BY INTERFERON GAMMA AND LIPOPOLYSACCHARIDE.  
 CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

```

CC -----
DR EMBL; D14051; BAA03138.1; -
DR EMBL; U26686; AAB85861.1; -
DR EMBL; U03699; AAC13747.1; -
DR EMBL; D12520; BAA02090.1; -
DR EMBL; L12562; AAA1720.1; -
DR EMBL; X76881; CAA54208.1; -
DR EMBL; D44591; BAA07994.1; -
DR EMBL; D83661; BAA12035.1; -
DR EMBL; AF006619; AAC16401.1; -
DR EMBL; U48829; AAB18620.1; -
DR EMBL; S71597; AAB31028.2; -
DR EMBL; L36063; AAC02242.1; -
DR PIR; JC1472; JCI1472.
DR HSSP; P29477; INOC.
DR InterPro; IPR001094; -
DR InterPro; IPR001433; -
DR InterPro; IPR001709; -
DR InterPro; IPR003037; -
DR Pfam; PF00667; FAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW Zinc; Metal-binding; Multigene family; Heme;
KW Zinc; Metal-binding; Multigene family.
FT BINDING 197 197
FT DOMAIN 506 526
FT NP_BIND 620 651
FT NP_BIND 764 775
FT NP_BIND 900 910
FT NP_BIND 975 993
FT NP_BIND 1073 1088
FT METAL 107 112
FT METAL 112 112
FT CONFLICT 10 10
FT CONFLICT 72 72
FT CONFLICT 107 107
FT CONFLICT 128 128
FT CONFLICT 130 130
FT CONFLICT 171 171
FT CONFLICT 195 195
FT CONFLICT 248 248
FT CONFLICT 264 264
FT CONFLICT 277 277
FT CONFLICT 348 348
FT CONFLICT 349 349
FT CONFLICT 380 380
FT CONFLICT 395 395
FT CONFLICT 412 412
FT CONFLICT 477 477
FT CONFLICT 513 513
FT CONFLICT 515 515
FT CONFLICT 545 545
FT CONFLICT 551 551
FT CONFLICT 556 556
FT CONFLICT 564 564
FT CONFLICT 570 570
FT CONFLICT 583 583
FT CONFLICT 591 591
FT CONFLICT 591 591
FT CONFLICT 619 619
FT CONFLICT 664 664
FT CONFLICT 679 680
FT CONFLICT 690 690
Query Match 83.5%; Score 81; DB 1; Length 1147;
Best Local Similarity 77.8%; Pred. No. 6.8e-06;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 RMTLVFGSRPDEDHQY 18
DB 1006 RMTLVFGSRPDEDHQY 1023

```

```

RESULT 5
NS2D_HUMAN STANDARD; PRT; 1147 AA.
ID NS2D_HUMAN
AC O60591; O60604;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE NITRIC OXIDE SYNTHASE, INDUCIBLE IID (EC 1.14.13.39) (NOS, TYPE II D)
DE (INDUCIBLE NOS) (INOS).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Skeletal muscle, and Heart muscle;
RX MEDLINE=99066690; PubMed=9851365;
RA Adams V., Krabbes S., Jlang H., Yu J., Rahmel A., Gielen S.,
RA Schuler G., Hambrecht R.;
RT "Complete coding sequence of inducible nitric oxide synthase from
RT human heart and skeletal muscle of patients with chronic heart
RT failure.";
RL Nitric Oxide 2:242-249(1998).
CC -|- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO
CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS. MAY BE INVOLVED IN
CC THE PATHOGENESIS OF DILATED CARDIOMYOPATHY OR OF EXERCISE
CC INTOLERANCE OBSERVED IN PATIENTS WITH CHRONIC HEART FAILURE.
CC -|- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +
CC NITRIC OXIDE + N NADP(+).
CC -|- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME (BY SIMILARITY).
CC -|- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (BY
CC SIMILARITY).
CC -|- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -|- TISSUE SPECIFICITY: EXPRESSED IN THE HEART AND SKELETAL MUSCLE
CC DURING CHRONIC HEART FAILURE, BUT NOT IN HEALTHY INDIVIDUALS.
CC -|- SIMILARITY: BELONGS TO THE NOS FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF049656; AAC83553.1; -
CC EMBL; AF051164; AAC83554.1; -
CC HSSP; P29477; INOC.
CC InterPro; IPR001094; -
CC InterPro; IPR001433; -
CC InterPro; IPR001709; -
CC InterPro; IPR003097; -
CC Pfam; PF00667; FAD_binding; 1.
CC Pfam; PF00175; oxidored_fad; 1.
CC PRINTS; PR00369; FLAVODOXIN.
CC PRINTS; PR00371; FPNCR.
KW Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;
KW Heme; Zinc; Metal-binding; Multigene family.
FT BINDING 197 197
FT DOMAIN 506 526
FT NP_BIND 620 651
FT NP_BIND 764 775
FT NP_BIND 900 910
FT NP_BIND 975 993
FT NP_BIND 1073 1088
FT METAL 107 107
FT METAL 112 112
FT CONFLICT 248 248
FT CONFLICT 248 248
N -> S (IN AAC83554).

```

FT CONFLICT 271 271 D -> A (IN AAC83554).  
 FT CONFLICT 399 399 G -> E (IN AAC83554).  
 FT CONFLICT 640 640 P -> Q (IN AAC83554).  
 FT CONFLICT 731 731 A -> T (IN AAC83554).  
 FT CONFLICT 937 937 H -> N (IN AAC83554).  
 FT CONFLICT 1008 1009 TL -> NF (IN AAC83554).  
 FT CONFLICT 1024 1024 E -> K (IN AAC83554).  
 FT CONFLICT 1076 1076 I -> L (IN AAC83554).  
 FT CONFLICT 1129 1129 F -> V (IN AAC83554).  
 SQ SEQUENCE 1147 AA; 130528 MW; FF7E4C7ABA76D820 CRC64;

Query Match 83.5%; Score 81; DB 1; Length 1147;

Best Local Similarity 77.8%; Pred.No. 6.8e-06;  
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RMTLVFGRPRDEHDHYQ 18  
 ||||| | | :||| :||  
 Db 1006 RMTLVFGRPRDEHDLYQ 1023

## RESULT

NOS2\_MOUSE  
 ID NOS2\_MOUSE STANDARD; PRT: 1144 AA.  
 AC P29477: 070515; 070516;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)  
 DE (INDUCIBLE NOS) (INOS) (MACROPHAGE NOS) (MAC-NOS).  
 OS NOS2 OR INOSL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92229444; PubMed=1373532;  
 RA Xie Q.-W., Cho H.J., Calaycay J., Mumford R.A., Swiderek K.M.,  
 Lee T.D., Ding A., Froso T., Nathan C.;  
 RT "Cloning and characterization of inducible nitric oxide synthase from  
 mouse macrophages.";  
 RL Science 256:225-228(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92357701; PubMed=1379716;  
 RA Lowenstein C.J., Glatt C.S., Bredt D.S., Snyder S.H.;  
 RT "Cloned and expressed macrophage nitric oxide synthase contrasts with  
 the brain enzyme.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92210618; PubMed=1372907;  
 RA Lyons C.R., Orloff G.J., Cunningham J.M.;  
 RT "Molecular cloning and functional expression of an inducible nitric  
 oxide synthase from a murine macrophage cell line.";  
 RL J. Biol. Chem. 267:6370-6374(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9608781; PubMed=7503239;  
 RA Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.;  
 RT "Role of NF-kappa B in the regulation of inducible nitric oxide  
 synthase in an MPA cell line";  
 RL Am. J. Physiol. 269:F718-F729(1995).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DBA/2J, BALB/cBYJ, SJL/J, NOD/LTJ, AND B10.S/J; TISSUE=Spleen;  
 RA Ma R.Z., Teuscher C.;  
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.  
 RX MEDLINE=97477482; PubMed=9334294;  
 RA Crane B.R., Arvai A.S., Gachhui R., Wu C., Ghosh D.K., Getzoff E.D.,

RA Stuehr D.J., Tainer J.A.;  
 RT "The structure of nitric oxide synthase oxygenase domain and  
 inhibitor complexes.";  
 RL Science 278:425-431(1997).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.  
 RX MEDLINE=20031637; PubMed=10562538;  
 RA Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C.,  
 Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.;  
 RA "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin  
 hook and pterin-binding segment in dimerization and  
 tetrahydrobiopterin interaction.";  
 RL EMBO J. 18:6260-6270(1999).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.  
 RX MEDLINE=98182450; PubMed=9516116;  
 RA Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,  
 Tainer J.A.;  
 RA "Structure of nitric oxide synthase oxygenase dimer with pterin and  
 substrate.";  
 RL Science 279:2121-2126(1998).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.  
 RX MEDLINE=20031638; PubMed=10562539;  
 RA Crane B.R., Rosenfeld R.J., Arvai A.S., Ghosh D.K., Ghosh S.,  
 Tainer J.A., Stuehr D.J., Getzoff E.D.;  
 RA "N-terminal domain swapping and metal ion binding in nitric oxide  
 synthase dimerization.";  
 RL EMBO J. 18:6271-6281(1999).  
 RN [10]  
 RP EFFECT OF ASPIRIN.  
 RC TISSUE=Macrophage;  
 RX MEDLINE=95372392; PubMed=7544010;  
 RA Amin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,  
 Weissmann G., Abramson S.B.;  
 RT "The mode of action of aspirin-like drugs: effect on inducible nitric  
 oxide synthase.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).  
 CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO  
 MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.  
 CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) -> CITRULLINE +  
 NITRIC OXIDE + N NADP(+).  
 CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 THE ENZYME.  
 CC -!- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN  
 INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE  
 EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL  
 MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY.  
 CC -!- SUBUNIT: HOMODIMER.  
 CC -!- TISSUE SPECIFICITY: MACROPHAGES.  
 CC -!- INDUCTION: BY TREATMENT WITH ENDOPOXINS OR CYTOKINES.  
 CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M87039; AAA39315.1; -;  
 DR EMBL; M92649; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; M84373; AAA39834.1; -;  
 DR EMBL; U43428; AAC52356.1; -;  
 DR EMBL; AF065919; AAC17914.1; -;  
 DR EMBL; AF065920; AAC17915.1; -;  
 DR EMBL; AF065921; AAC17916.2; -;  
 DR EMBL; AF065922; AAC17917.1; ALT\_INIT.  
 DR EMBL; AF065923; AAC17918.2; -;  
 DR PIR; A43271; A43271.

```

DR PIR: A42166; A42166.
DR PDB: INOC; 18-NOV-98.
DR PDB: INOS; 18-NOV-98.
DR PDB: 2NOS; 18-NOV-98.
DR PDB: INOD; 23-MAR-99.
DR PDB: 2NOD; 23-MAR-99.
DR PDB: 3NOD; 23-MAR-99.
DR PDB: 1DF1; 08-DEC-99.
DR PDB: 1DMV; 04-FEB-00.
DR PDB: 1DMW; 06-FEB-00.
DR PDB: 1DWX; 06-FEB-00.
DR PDB: 1DOM; 15-DEC-99.
DR PDB: 1DD7; 29-MAR-00.
DR MGD; MGI: 97361; NOS2.
DR InterPro: IPR001094; -.
DR InterPro: IPR001433; -.
DR InterPro: IPR001709; -.
DR InterPro: IPR003097; -.
DR Pfam: PF00667; FAD_binding; 1.
DR Pfam: PF00175; oxidoreductase; 1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
KW Zinc; Metal-binding; Multigene family; 3D-structure.
FT BINDING 194 194
FT DOMAIN 503 523
FT NP_BIND 617 648
FT NP_BIND 761 772
FT NP_BIND 897 907
FT NP_BIND 972 980
FT NP_BIND 1070 1085
FT METAL 104 104
FT METAL 109 109
FT VARIANT 211 211
FT VARIANT 967 967
FT VARIANT 968 968
FT CONFLICT 19 19
FT CONFLICT 191 191
FT CONFLICT 844 844
FT SEQUENCE 1144 AA; 130574 MW; 0735BE676113457F CRC64;

Query Match 79.4%; Score 77; DB 1; Length 1144;
Best Local Similarity 72.2%; Pred. No. 3.3e-05;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RMTLVFGSRPPDEHLYQ 18
DB 1003 RMTLVFGSRPPDEHLYQ 1020

RESULT 7
NS2_CAVPO STANDARD; PRT; 1149 AA.
AC 054705;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)
DE (INDUCIBLE NOS) (INOS).
GN NOS2 OR NOS.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=HARTLEY; TISSUE=Lung;
RX MEDLINE=98343971; PubMed=9677342;
RA Shirato M., Sakamoto T., Uchida Y., Nomura A., Ishii Y., Iijima H.,
RA Goto Y., Hasegawa S.;
RT "Molecular cloning and characterization of Ca2+-dependent inducible
nitric oxide synthase from guinea-pig lung.";

RL Biochem. J. 333:795-799(1998).
CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.
CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +
NITRIC OXIDE + N NADP(+).
CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
THE ENZYME (BY SIMILARITY).
CC -!- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST
WITH MOUSE NOS2).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE LUNG AND COLON. NOT DETECTED
IN THE HEART, AORTA, LIVER, KIDNEY, AND SPLEEN.
CC -!- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS) IN KIDNEY, SPLEEN, AND
COLON. EXPRESSION IS REDUCED IN THE PRESENCE OF LPS IN LUNG.
CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF027180; AAC33177.1; -.
CC HSP: P29477; 2NOS.
CC InterPro: IPR001094; -.
CC InterPro: IPR001433; -.
CC InterPro: IPR001709; -.
CC InterPro: IPR003097; -.
CC Pfam: PF00667; FAD_binding; 1.
CC Pfam: PF00175; oxidoreductase; 1.
CC PRINTS: PR00369; FLAVODOXIN.
CC PRINTS: PR00371; FPNCR.
KW Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;
KW Heme; Multigene family.
FT BINDING 199 199
FT DOMAIN 508 528
FT NP_BIND 622 653
FT NP_BIND 766 777
FT NP_BIND 902 912
FT NP_BIND 977 995
FT NP_BIND 1075 1090
FT SEQUENCE 1149 AA; 130631 MW; 66D595A2486DB50E CRC64;

Query Match 78.4%; Score 76; DB 1; Length 1149;
Best Local Similarity 72.2%; Pred. No. 4.8e-05;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RMTLVFGSRPPDEHLYQ 18
DB 1008 RMTLVFGSRPPDEHLYQ 1025

RESULT 8
NS2B_HUMAN STANDARD; PRT; 79 AA.
AC P81272;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NITRIC-OXIDE SYNTHASE IIB (EC 1.14.13.39) (NOS, TYPE II B) (NOSIIB)
DE (FRAGMENTS).
GN NOS2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;

```

RX MEDLINE=96047340; PubMed=7558036;  
 RA Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G.,  
 Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;  
 RT "Three members of the nitric oxide synthase II gene family (NOS2A,  
 NOS2B, and NOS2C) colocalize to human chromosome 17.";  
 RL Genomics 27:526-530(1995).  
 CC -|- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO  
 MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.  
 CC -|- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) -> CITRULLINE +  
 NITRIC OXIDE + N NADP(+).  
 CC -|- COPACITOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 THE ENZYME (BY SIMILARITY).  
 CC -|- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (BY  
 SIMILARITY).  
 CC -|- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -|- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation  
 at the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; U18332; AAC50232.1; -;  
 DR EMBL; U18333; AAC50233.1; -;  
 DR HSSP; P00388; IAMO.  
 DR MIM; 600719; -;  
 KW Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;  
 KW Heme; Multigene family.  
 FT NON\_TER 1  
 FT NP\_BIND 15 >30 NADP (RIBOSE PART) (BY SIMILARITY).  
 FT NON\_CONS 30 31  
 FT NON\_TER 79 79  
 SQ SEQUENCE 79 AA; 8667 MW; 83705AEOC36A94E0 CRC64;

Query Match 68.0%; Score 66; DB 1; Length 79;

Best Local Similarity 72.2%; Pred. NO. 0.00014;

Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RMTLVFGSRPDEHIYQ 18

Db 35 RMTVPFECSPNEDHIYQ 52

RESULT 9

NOS2\_CHICK  
 ID NOS2\_CHICK STANDARD; PRT; 1136 AA.  
 AC Q90703; Q90677; Q90934;  
 DT 01-NOV-1997 (Rel. 35; Created)  
 DT 01-NOV-1997 (Rel. 35; Last sequence update)  
 DT 30-MAY-2000 (Rel. 39; Last annotation update)  
 DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)  
 DE (INDUCIBLE NOS) (INOS) (MACROPHAGE NOS).  
 GN NOS2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96216113; PubMed=8662618;  
 RA Lin A.W., Chang C.C., McCormick C.C.;  
 RT "Molecular cloning and expression of an avian macrophage nitric-oxide  
 synthase cDNA and the analysis of the genomic 5'-flanking region.";  
 RL J. Biol. Chem. 271:11911-11919(1996).  
 RN [2]  
 RP SEQUENCE OF 171-472 FROM N.A.

RC TISSUE=Osteoclast;  
 RX MEDLINE=96252270; PubMed=8707887;  
 RA Sunyer T., Rothe L., Jiang X., Osobdy P., Collin-Osdoby P.;  
 RT "Proinflammatory agents, IL-8 and IL-10, upregulate inducible nitric  
 oxide synthase expression and nitric oxide production in avian  
 osteoclast-like cells.";  
 RL J. Cell. Biochem. 60:469-483(1996).  
 RN [3]  
 RP SEQUENCE OF 646-986 FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=98375063; PubMed=9709401;  
 RA Shimizu T., Kinugawa K., Sugishita Y., Sugishita K., Harada K.,  
 Matsui H., Kohmoto O., Serizawa T., Takahashi T.;  
 RT "Molecular cloning and expression of inducible nitric oxide synthase  
 in chick embryonic ventricular myocytes.";  
 RL Cardiovasc. Res. 38:403-413(1998).  
 CC -|- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. NO MAY SERVE AS BOTH A  
 PARACRINE AND AUTOCRINE SIGNAL FOR MODULATING OSTEOCLAST BONE  
 RESORPTION.  
 CC -|- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) -> CITRULLINE +  
 NITRIC OXIDE + N NADP(+).  
 CC -|- COPACITOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 THE ENZYME (BY SIMILARITY).  
 CC -|- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN.  
 CC -|- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -|- INDUCTION: BY TREATMENT WITH LIPOPOLYSACCHARIDES (LPS) OR  
 CYTOKINES, BUT NOT IN OSTEOCLASTS WHERE THEY ARE INDUCED BY  
 CALCIUM AND PMA (PHORBOL 12-MYRISTATE 13-ACETATE).  
 CC -|- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation  
 at the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; U46504; AAC59886.1; -;  
 DR EMBL; U34045; AAB17499.1; -;  
 DR EMBL; D85422; BAA12817.1; -;  
 DR HSSP; P00388; IAMO.  
 DR InterPro; IPR001094; -;  
 DR InterPro; IPR001433; -;  
 DR InterPro; IPR001709; -;  
 DR InterPro; IPR003097; -;  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR PRINTS; PR00175; oxidored\_fad; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme; Zinc;  
 KW Metal-binding.  
 FT BINDING 197 197 HEME (BY SIMILARITY).  
 FT DOMAIN 506 526 CALMODULIN-BINDING (POTENTIAL).  
 FT NP\_BIND 620 651 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FT NP\_BIND 764 775 FAD (ADP PART) (BY SIMILARITY).  
 FT NP\_BIND 900 910 FAD (FLAVIN PART) (BY SIMILARITY).  
 FT NP\_BIND 975 993 NADP (RIBOSE PART) (BY SIMILARITY).  
 FT NP\_BIND 1073 1088 NADP (ADP PART) (BY SIMILARITY).  
 FT METAL 107 107 ZINC (BY SIMILARITY).  
 FT METAL 112 112 ZINC (BY SIMILARITY).  
 FT CONFLICT 400 400 S -> T (IN REF. 2).  
 FT CONFLICT 873 873 R -> S (IN REF. 3).  
 SQ SEQUENCE 1136 AA; 129649 MW; D5CB73AC7BA94B9D CRC64;

Query Match 63.9%; Score 62; DB 1; Length 1136;

Best Local Similarity 64.7%; Pred. NO. 0.012;

Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MTLVFGSRPDEHIYQ 18



```

Db 1007 MILLFGCRHPDMDHIYK 1023
      | | | | | | | | | |
RESULT 10
NS2C_HUMAN STANDARD; PRT; 69 AA.
AC Q14961;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE NITRIC-OXIDE SYNTHASE IIC (EC 1.14.13.39) (NOS, TYPE II C) (NOSIIC)
DE (FRAGMENT).
GN NOS2C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE=96047340; PubMed=7558036;
RA Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G.,
RA Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;
RT "Three members of the nitric oxide synthase II gene family (NOS2A,
RT NOS2B, and NOS2C) colocalize to human chromosome 17."
RL Genomics 27:526-530(1995).
CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO
CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.
CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +
CC NITRIC OXIDE + N NADP(+).
CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME (BY SIMILARITY).
CC -!- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (BY
CC SIMILARITY).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U18335; AAC50245.1; -
DR EMBL; U18334; AAC50245.1; JOINED.
DR HSP; P00388; IAMO.
DR MIM; 600720; -.
KW Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;
FT NON_TER 1 1 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 7 25
FT NON_BIND 69 69
FT NON_TER 1 1
FT SEQUENCE 69 AA; 8432 MW; 2C29D595F93FB293 CRC64;
SQ
      Query Match 60.8%; Score 59; DB 1; Length 69;
      Best Local Similarity 66.7%; Pred. No. 0.0019; Mismatches 5; Indels 0; Gaps 0;
      Matches 12; Conservative 1;
QY 1 RMTLVFGSRPPDDEHIYQ 18
      | | | | | | | | | |
Db 38 RRTLVFWCRPPDDEHIYR 55
      | | | | | | | | | |
RESULT 11
CYPE_BACSU STANDARD; PRT; 1054 AA.
AC O08336;

```

```

DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE BIFUNCTIONAL P-450:NADPH-P450 REDUCTASE 2 [INCLUDES:
DE CYTOCHROME P450 102 (EC 1.14.14.1); NADPH-CYTOCHROME P450 REDUCTASE
DE (EC 1.6.2.4)].
GN CYPE OR CYP102A3.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
ON NCBI_TaxID=1423;
RX MEDLINE=97453479; PubMed=9308178;
RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
RA Duesterhoeft A., Ehrlich S.D.;
RT "Sequence of the Bacillus subtilis genome region in the vicinity of
RT the lev operon reveals two new extracytoplasmic function RNA
RT polymerase sigma factors Sigv and SigZ."
RL Microbiology 143:2939-2943(1997).
CC -!- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE
CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
CC P450 (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME = NADP(+) +
CC 2 FERROCYTOCHROME.
CC -!- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FMN (BY SIMILARITY).
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
CC P450 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U93874; AAB80867.1; -
DR EMBL; Z99117; CAB14658.1; -
DR HSP; P14779; IFAG.
DR Subtilist; BG12299; cyPE.
DR InterPro; IPR001128; -
DR InterPro; IPR001433; -
DR InterPro; IPR001709; -
DR InterPro; IPR002402; -
DR InterPro; IPR003097; -
DR Pfam; PF00067; p450; 1.
DR Pfam; PF00175; oxidored_fad; 1.
DR Pfam; PF00667; FAD_binding; 1.
DR PRINTS; PR00371; FPNCR.
DR PRINTS; PR00385; P450.
DR PRINTS; PR00464; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP.
FT DOMAIN 1 475 CYTOCHROME P450.
FT BINDING 472 1053 NADPH-P-450 REDUCTASE.
FT BINDING 403 403 HEME (BY SIMILARITY).
FT SEQUENCE 1054 AA; 118675 MW; 705F8E27866C110 CRC64;
SQ
      Query Match 53.6%; Score 52; DB 1; Length 1054;
      Best Local Similarity 60.0%; Pred. No. 0.54;
      Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
      Matches 937 LVFGSRPPDDEHIYQ 18
      | | | | | | | | | |
QY 4 LVFGSRPPDDEHIYQ 18
      | | | | | | | | | |
Db 937 LVFGSRPPDDEHIYR 951
      | | | | | | | | | |
RESULT 12
NOS3_RAT

```

```

ID NOS3_RAT STANDARD; PRT; 919 AA.
AC Q62600; O88672; O89041; Q62734;
DT 01-NOV-1997 (Rel. 35; Created)
DT 30-MAY-2000 (Rel. 39; Last sequence update)
DT 30-MAY-2000 (Rel. 39; Last annotation update)
DE NITRIC-OXIDE SYNTHASE, ENDOTHELIAL (EC 1.14.13.39) (EC-NOS) (NOS, TYPE
DE III) (NOSIII) (ENDOTHELIAL NOS) (ENOS) (CONSTITUTIVE NOS) (CNOS)
DE (FRAGMENTS).
GN NOS3.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
[1]
RP STRAIN-SPRAGUE-DAWLEY;
RC Toporsian M., Govindaraju K., Nagi M., Eldelman D., Thibault G.,
RA Ward M.E.;
RT "Downregulation of endothelial nitric oxide synthase (NOS III) in rat
RT aorta following in-vivo hypoxia.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 288-487 AND 678-919 FROM N.A.
RC TISSUE=Brain;
RA Seigel B., Jiang L., Wolf G.;
RT "Cloning and expression of the rat endothelial nitric oxide
RT synthase.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 448-677 FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE=95089280; PubMed=7527874;
RA Mohaupt M.G., Elzie J.L., Ahn K.Y., Clapp W.L., Wilcox C.S.,
RA Kone B.C.;
RT "Differential expression and induction of mRNAs encoding two
RT inducible nitric oxide synthases in rat kidney.";
RL Kidney Int. 46:653-665(1994).
RN [4]
RP SEQUENCE OF 742-859 FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Lung;
RA Minchenko A.G., Armstead V.E., Opentanova I.L., Lefer A.M.;
RT "Endothelin-1, endothelin receptors and eCNOS mRNA expression in
RT vital organs during traumatic shock in rats.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 745-807 FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Lung;
RX MEDLINE=95250990; PubMed=7537461;
RA Kawai N., Bloch D.B., Filippov G., Rabkina D., Suen H.C., Losty P.D.,
RA Janssens S.P., Zapol W.M., de la Monte S., Bloch K.D.;
RT "Constitutive endothelial nitric oxide synthase gene expression is
RT regulated during lung development.";
RL Am. J. Physiol. 268:L589-L595(1995).
CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN
CC VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A GMP-MEDIATED SIGNAL
CC TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH
CC FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND
CC PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS.
CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +
CC NITRIC OXIDE + N NADP(+).
CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME.
CC -!- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY
CC SIMILARITY).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED CONSTITUTIVELY BY VASCULAR
CC ENDOTHELIUM. DETECTED IN ALVEOLAR AND SEROSAL EPITHELIAL CELLS AS
CC WELL AS IN ENDOTHELIAL CELLS IN ONE DAY OLD RAT. IN ADULT LUNG,
CC DETECTED IN RARE ENDOTHELIAL CELLS.
CC -!- DEVELOPMENTAL STAGE: DETECTED AT HIGH LEVELS IN LUNG DURING THE
CC LATE FETAL AND POSTNATAL PERIOD AND AT LOWER LEVELS IN ADULT.
CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.

-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
CC EMBL; AF085195; AAC34677.1; -
CC EMBL; AJ011115; CAA09493.1; -
CC EMBL; U02534; AAA96141.1; -
CC EMBL; AJ011116; CAA09494.1; -
CC EMBL; AF093837; AAC64178.1; -
CC DR EMBL; U18336; AAC52188.1; -
CC DR HSP; P29477; INOC
CC InterPro; IPR003097; -
CC Pfam; PF00667; FAD_binding; 1.
CC PRINTS; PR00369; FLAVODOXIN.
CC PRINTS; PR00371; FPNCR.
CC Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;
KW Lipoprotein; Palmitate; Calcium-binding; Heme; Zinc; Metal-binding;
KW Multigene family.
KW INIT_MET 0
FT BINDING 182 182 BY SIMILARITY.
FT NON_CONS 287 288 HEME (BY SIMILARITY).
FT DOMAIN 304 324 CALMODULIN-BINDING (POTENTIAL).
FT NP_BIND 463 494 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 607 618 FAD (ADP PART) (BY SIMILARITY).
FT NON_CONS 677 678 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 736 754 NADP (ADP PART) (BY SIMILARITY).
FT NP_BIND 834 849 MYRISTATE (BY SIMILARITY).
FT LIPID 1 14 PALMITATE (BY SIMILARITY).
FT LIPID 25 25 PALMITATE (BY SIMILARITY).
FT METAL 92 92 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT NON_TER 919 919
SQ SEQUENCE 919 AA; 101404 MW; BF2EAC391C86650F CRC64;

Query Match 52.6%; Score 51; DB 1; Length 919;
Best Local Similarity 58.8%; Pred. No. 0.69;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTLVFGSRPRDEHIYQ 18
Db 768 MTLVFGRCRCSQLDHLR 784

RESULT 13
CPXB_BACME STANDARD; PRT; 1048 AA.
AC P14779;
DT 01-APR-1990 (Rel. 14; Created)
DT 01-APR-1990 (Rel. 14; Last sequence update)
DT 01-OCT-2000 (Rel. 40; Last annotation update)
DE BIFUNCTIONAL P-450:NADPH-P450 REDUCTASE (CYTOCHROME P450(BM-3))
DE (P450BM-3) [INCLUDES: CYTOCHROME P450 102 (EC 1.14.14.1); NADPH-
DE CYTOCHROME P450 REDUCTASE (EC 1.6.2.4)].
DE CYP102A1 OR CYP102.
GN Cytochrome megaterium.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxId=1404;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89291834; PubMed=2544578;
RA Ruettinger R.T., Wen L.-P., Fulco A.J.;
RT "Coding nucleotide, 5' regulatory, and deduced amino acid sequences
RT of P-450BM-3, a single peptide cytochrome P-450:NADPH-P-450
RT reductase from Bacillus megaterium.";
RL J. Biol. Chem. 264:10987-10995(1989).
```

```

[2]
RN RP CHARACTERIZATION.
RX MEDLINE=92088245; PubMed=1727637;
RA Boddupalli S.S., Pramanik B.C., Slaughter C.A., Estabrook R.W.,
RA Peterson J.A.;
RT "Fatty acid monooxygenation by P450BM-3: product identification and
RT proposed mechanisms for the sequential hydroxylation reactions.";
RL Arch. Biochem. Biophys. 292:20-28(1992).
[3]
RN RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-471.
RX MEDLINE=93342510; PubMed=8342039;
RA Ravichandran K.G., Boddupalli S.S., Hasemann C.A., Peterson J.A.,
RA Deisenhofer J.;
RT "Crystal structure of hemoprotein domain of P450BM-3, a prototype for
RT microsomal P450's";
RL Science 261:731-736(1993).
[4]
RN RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-471.
RX MEDLINE=97185914; PubMed=9033595;
RA Li H.Y., Poulos T.L.;
RT "The structure of the cytochrome P450BM-3 haem domain complexed with
RT the fatty acid substrate, palmitoleic acid.";
RL Nat. Struct. Biol. 4:140-146(1997).
[5]
RN RP X-RAY CRYSTALLOGRAPHY (2.03 ANGSTROMS).
RX MEDLINE=99162523; PubMed=10051560;
RA Sevriloukova I.F., Li H., Zhang H., Peterson J.A., Poulos T.L.;
RT "Structure of a cytochrome P450-redox partner electron-transfer
RT complex.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1863-1868(1999).
CC CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. CATALYSES
CC -1- HYDROXYLATION OF MEDIUM AND LONG-CHAIN FATTY ACIDS AT OMEGA-1,
CC OMEGA-2 AND OMEGA-3 POSITIONS, WITH OPTIMUM CHAIN LENGTHS OF 14-16
CC CARBONS (LAURIC, MYRISTIC, AND PALMITIC ACIDS). THE REDUCTASE
CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
CC P450.
CC CC -1- CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME = NADP(+) +
CC 2 FERROCYTOCHROME.
CC CC -1- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FMN.
CC CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
CC P450 FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; J04832; AAA87602.1; -.
DR PIR; A34286; A34286.
DR PDB; 2HPD; 31-OCT-93.
DR PDB; 2BMH; 31-JUL-94.
DR PDB; 1FAG; 12-FEB-97.
DR PDB; 1FAH; 12-FEB-97.
DR PDB; 1B07; 23-SEP-98.
DR PDB; 1BVI; 23-FEB-99.
DR InterPro; IPR001128; -.
DR InterPro; IPR001433; -.
DR InterPro; IPR001709; -.
DR InterPro; IPR002402; -.
DR InterPro; IPR003097; -.
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00175; oxidored_fad; 1.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00371; FPNCR.
DR PRINTS; PR00385; P450.
DR PRINTS; PR00464; EP450II.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Multifunctional enzyme; FMN; FAD; Flavoprotein; 3D-structure; NADP.
FT INIT MET 0 0

```

```
RESULT 14
NOS3 MOUSE
ID NOS3 MOUSE STANDARD; PRT; 1201 AA.
AC P70313; O505056;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NITRIC-OXIDE SYNTHASE, ENDOTHELIAL (EC 1.14.13.39) (EC-NOS) (NOS, TYPE
III) (NOSIII) (ENDOTHELIAL NOS) (ENOS) (CONSTITUTIVE NOS) (CNOS).
GN NOS3 OR ECNOS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal heart;
RX MEDLINE=96350460; PubMed=8764825;
RA Gnanapandithen K., Chen Z., Kau C.-L., Gorczynski R.M., Marsden P.A.;
RT "Cloning and characterization of murine endothelial constitutive
nitric oxide synthase."
RL Biochim. Biophys. Acta 1308:103-106(1996).
RN [2]
RP SEQUENCE OF 1-53 FROM N.A.
RC TISSUE=Fetal heart;
RA Gregg A.R., Schauer A., Shi O., Liu Z., Lee C.G.L., O'Brien W.E.;
RT "Limb reduction defects in endothelial nitric oxide synthase deficient
mice."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION.
RX MEDLINE=99061722; PubMed=9843834;
RA Gregg A.R., Schauer A., Shi O., Liu Z., Lee C.G.L., O'Brien W.E.;
RT "Limb reduction defects in endothelial nitric oxide synthase-deficient
mice."
RL Am. J. Physiol. 275:H2319-H2324(1998).
CC -|- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN
CC VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A CGMP-MEDIATED SIGNAL
CC TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH
CC FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND
CC PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS. MAY
CC PLAY A SIGNIFICANT ROLE IN NORMAL AND ABNORMAL LIMB DEVELOPMENT.
CC -|- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) -> CITRULLINE +
CC NITRIC OXIDE + N NADP(+).
CC -|- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME.
CC -|- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY
CC SIMILARITY).
CC -|- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE NOS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U53142; AAC52766.1; -.
CC DR EMBL; AF045940; AAC02553.1; -.
CC DR HSSP; P29477; 2NOS.
CC DR MGD; MGI:97362; Nos3.
CC DR InterPro; IPR001094; -.
CC DR InterPro; IPR001433; -.
CC DR InterPro; IPR001709; -.
CC DR InterPro; IPR003097; -.
CC DR Pfam; PF00175; oxidored_fad; 1.
CC DR Pfam; PF00667; fad_binding; 1.
CC DR PRINTS; PR00369; FLAVODOXIN.
CC DR PRINTS; PR00371; FPNCR.
```

```
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;
KW Lipoprotein; Palmitate; Calcium-binding; Heme; Zinc; Metal-binding;
KW Multigene family.
FT INIT_MET 0 BY SIMILARITY.
FT BINDING 182 182 HEME (BY SIMILARITY).
FT DOMAIN 489 508 CALMODULIN-BINDING (POTENTIAL).
FT NP_BIND 647 678 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 791 802 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 933 943 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 1008 1026 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 1106 1121 NADP (ADP PART) (BY SIMILARITY).
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
FT LIPID 14 14 PALMITATE (BY SIMILARITY).
FT LIPID 25 25 PALMITATE (BY SIMILARITY).
FT METAL 92 92 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT CONFLICT 49 49 A -> P (IN REF. 2).
SQ SEQUENCE 1201 AA; 132748 MW; DA37ABAC947DABD5 CRC64;

Query Match 52.6%; Score 51; DB 1; Length 1201;
Best Local Similarity 58.8%; Pred. No. 0.92;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTLVFGSRPRDDEHIYQ 18
IIIIII I III:
Db 1040 MTLVFGCRCSQLDHLR 1056

RESULT 15
NOS3 HUMAN
ID NOS3 HUMAN STANDARD; PRT; 1202 AA.
AC P29474; Q14251; Q1434; Q13662;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NITRIC-OXIDE SYNTHASE, ENDOTHELIAL (EC 1.14.13.39) (EC-NOS) (NOS, TYPE
III) (NOSIII) (ENDOTHELIAL NOS) (ENOS) (CONSTITUTIVE NOS) (CNOS).
GN NOS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92340475; PubMed=1378832;
RA Janssens S.P., Shimouchi A., Quertermous T., Bloch D.B., Bloch K.D.;
RT "Cloning and expression of a cDNA encoding human endothelium-derived
relaxing factor/nitric oxide synthase."
RL J. Biol. Chem. 267:14519-14522(1992).
RN [2]
RP ERRATUM.
RA Janssens S.P., Shimouchi A., Quertermous T., Bloch D.B., Bloch K.D.;
RL J. Biol. Chem. 267:22694-22694(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92354731; PubMed=1379542;
RA Marsden P.A., Schaperk K.T., Chen H.S., Flowers M., Sundell C.L.,
Wilcox J.N., Lamas S., Michel T.;
RT "Molecular cloning and characterization of human endothelial nitric
oxide synthase."
RL FEBS Lett. 307:287-293(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93352539; PubMed=7688726;
RA Marsden P.A., Heng H.H., Scherer S.W., Stewart R.J., Hall A.V.,
Shi X.M., Tsui L.C., Schappert K.T.;
RT "Structure and chromosomal localization of the human constitutive
endothelial nitric oxide synthase gene."
RL J. Biol. Chem. 268:17478-17488(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein;
```

RA Liao J.K.;  
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=94161710; PubMed=7509596;  
RA Nadaud S.A., Bonnardaux A., Lathrop M., Soubrier F.;  
RT "Gene structure, polymorphism and mapping of the human endothelial  
RL nitric oxide synthase gene.";  
RL Biochem. Biophys. Res. Commun. 198:1027-1033(1994).  
RN [7]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94333373; PubMed=7519987;  
RA Miyahara K., Kawamoto T., Sase K., Yui Y., Toda K., Yang L.X.,  
RA Hattori R., Aoyama T., Yamamoto Y., Doi Y., Ogoshi S.,  
RA Hashimoto K., Kawai C., Sasayama S., Shizuta Y.;  
RT "Cloning and structural characterization of the human endothelial  
RL nitric-oxide-synthase gene.";  
RL Eur. J. Biochem. 223:719-726(1994).  
RN [8]  
RP SEQUENCE OF 1-52 FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=94245207; PubMed=7514568;  
RA Robinson L.J., Weremowicz S., Morton C.C., Michel T.;  
RT "Isolation and chromosomal localization of the human endothelial  
RL nitric oxide synthase (NOS3) gene.";  
RL Genomics 19:350-357(1994).  
RN [9]  
RP SEQUENCE OF 410-527 FROM N.A.  
RC TISSUE=Platelet;  
RX MEDLINE=96077182; PubMed=7475956;  
RA Sase K., Michel T.;  
RT "Expression of constitutive endothelial nitric oxide synthase in human  
RL blood platelets.";  
RL Life Sci. 57:2049-2055(1995).  
RN [10]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
RX MEDLINE=99173237; PubMed=10074942;  
RA Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,  
RA Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,  
RA Weber P.C.;  
RT "Structural characterization of nitric oxide synthase isoforms  
RL reveals striking active-site conservation.";  
RL Nat. Struct. Biol. 6:233-242(1999).  
RN [11]  
RP VARIANT CORONARY SPASM ASP-297.  
RX MEDLINE=98407797; PubMed=9737779;  
RA Yoshimura M., Yasue H., Nakayama M., Shimasaki Y., Sumida H.,  
RA Sugiyama S., Kugiyama K., Ogawa H., Ogawa Y., Saito Y., Miyamoto Y.,  
RA Nakao K.;  
RT "A missense Glu298Asp variant in the endothelial nitric oxide synthase  
RL gene is associated with coronary spasm in the Japanese.";  
RL Hum. Genet. 103:65-69(1998).  
CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN  
CC VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A cGMP-MEDIATED SIGNAL  
CC TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH  
CC FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND  
CC PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS.  
CC -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +  
CC NITRIC OXIDE + N NADP(+).  
CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
CC TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
CC THE ENZYME.  
CC -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- TISSUE SPECIFICITY: PLATELETS.  
CC -1- DISEASE: DEFECTS IN NOS3 ARE INVOLVED IN CORONARY SPASM.  
CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M93718; AAA36364.1; -  
DR EMBL; M95296; AAA36372.1; -  
DR EMBL; L10709; AAA36365.1; -  
DR EMBL; L10693; AAA36385.1; JOINED.  
DR EMBL; L10694; AAA36365.1; JOINED.  
DR EMBL; L10695; AAA36365.1; JOINED.  
DR EMBL; L10696; AAA36365.1; JOINED.  
DR EMBL; L10697; AAA36365.1; JOINED.  
DR EMBL; L10698; AAA36365.1; JOINED.  
DR EMBL; L10699; AAA36385.1; JOINED.  
DR EMBL; L10700; AAA36365.1; JOINED.  
DR EMBL; L10701; AAA36365.1; JOINED.  
DR EMBL; L10702; AAA36365.1; JOINED.  
DR EMBL; L10703; AAA36365.1; JOINED.  
DR EMBL; L10704; AAA36365.1; JOINED.  
DR EMBL; L10705; AAA36365.1; JOINED.  
DR EMBL; L10706; AAA36365.1; JOINED.  
DR EMBL; L10707; AAA36365.1; JOINED.  
DR EMBL; L10708; AAA36365.1; JOINED.  
DR EMBL; L26914; AAA36374.1; -  
DR EMBL; X76303; CAA53950.1; -  
DR EMBL; X76304; CAA53950.1; JOINED.  
DR EMBL; X76305; CAA53950.1; JOINED.  
DR EMBL; X76306; CAA53950.1; JOINED.  
DR EMBL; X76307; CAA53950.1; JOINED.  
DR EMBL; X76308; CAA53950.1; JOINED.  
DR EMBL; X76309; CAA53950.1; JOINED.  
DR EMBL; X76310; CAA53950.1; JOINED.  
DR EMBL; X76311; CAA53950.1; JOINED.  
DR EMBL; X76312; CAA53950.1; JOINED.  
DR EMBL; X76313; CAA53950.1; JOINED.  
DR EMBL; X76314; CAA53950.1; JOINED.  
DR EMBL; X76315; CAA53950.1; JOINED.  
DR EMBL; X76316; CAA53950.1; JOINED.  
DR EMBL; D26607; BAA05652.1; -  
DR EMBL; L23210; AAA36373.1; -  
DR EMBL; S80791; AAD14336.1; -  
DR PIR; S24052; S24052.  
DR PIR; A42867; A42867.  
DR FDB; 3NOS; 04-FEB-00.  
DR MIM; 163729; -  
DR InterPro; IPR001094; -  
DR InterPro; IPR001433; -  
DR InterPro; IPR001709; -  
DR InterPro; IPR003037; -  
DR Pfam; PF00667; FAD\_binding; 1.  
DR PRINTS; PR00369; oxidored\_fad; 1.  
DR PRINTS; PR00371; FPNCR.  
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;  
KW Lipoprotein; Palmitate; Disulfide mutation; Calcium-binding; Heme;  
KW Zinc; Metal-binding; Multigene family; 3D-structure.  
FT INIT\_MET 0  
FT BINDING 183 183 HEME (BY SIMILARITY).  
FT DOMAIN 490 509 CALMODULIN-BINDING (POTENTIAL).  
FT NP\_BIND 648 679 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
FT NP\_BIND 792 803 FAD (ADP PART) (BY SIMILARITY).  
FT NP\_BIND 934 944 FAD (FLAVIN PART) (BY SIMILARITY).  
FT NP\_BIND 1009 1027 NADP (RIBOSE PART) (BY SIMILARITY).  
FT NP\_BIND 1107 1122 NADP (ADP PART) (BY SIMILARITY).  
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).  
FT LIPID 14 14 PALMITATE (BY SIMILARITY).  
FT LIPID 25 25 PALMITATE (BY SIMILARITY).  
FT METAL 93 93 ZINC.  
FT METAL 98 98 ZINC.  
FT VARIANT 297 297 E -> D (IN CORONARY SPASM).  
FT CONFLICT 52 52 /FTId=VAR\_008037.  
FT CONFLICT 488 488 S -> R (IN REF. 8).  
FT CONFLICT 488 488 G -> S (IN REF. 9).

FT CONFLICT 566 566 V -> W (IN REF. 6).  
FT CONFLICT 1149 1149 R -> RQ (IN REF. 7).  
FT CONFLICT 1193 1193 D -> E (IN REF. 6).  
SQ SEQUENCE 1202 AA; 133157 MW; 93D127D6C14AC92E CRC64;

Query Match 52.6%; Score 51; DB 1; Length 1202;  
Best Local Similarity 58.8%; Pred. No. 0.92;  
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTLVFGSRRPDEDEHIYQ 18  
||||| |  
Db 1041 MTLVFGRCRCSQLDHLVR 1057

Search completed: September 10, 2001, 14:09:54  
Job time: 563 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:01:15 ; Search time 42.28 Seconds  
(without alignments)  
32.430 Million cell updates/sec

Title: US-08-833-506c-31

Perfect score: 97  
Sequence: 1 RWLVFGSRPDEDHIVQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	94.8	1153	2 A49676	nitric-oxide synth
2	81	83.5	136	2 I46074	nitric-oxide synth
3	81	83.5	1147	1 S47647	nitric-oxide synth
4	81	83.5	1147	1 I56575	nitric-oxide synth
5	81	83.5	1147	1 S38253	nitric-oxide synth
6	81	83.5	1147	1 I53165	nitric-oxide synth
7	81	83.5	1147	2 JC5029	nitric-oxide synth
8	81	83.5	1147	2 S65440	nitric-oxide synth
9	77	79.4	1144	1 A43271	nitric-oxide synth
10	69	71.1	1147	2 JC5027	nitric-oxide synth
11	69	71.1	1147	2 JC5028	nitric-oxide synth
12	66	68.0	49	2 I38067	nitric-oxide synth
13	59	60.8	69	2 I39204	cytochrome P450 /
14	52	53.6	1054	1 A69975	cytochrome P450 /
15	51	52.6	63	2 I51917	nitric-oxide synth
16	51	52.6	1049	1 A34286	cytochrome P450 BM
17	51	52.6	1202	2 S71424	nitric-oxide synth
18	51	52.6	1203	1 A47501	nitric-oxide synth
19	51	52.6	1205	1 A38943	nitric-oxide synth
20	51	52.6	1429	2 JN0609	nitric-oxide synth
21	51	52.6	1429	2 S16233	nitric-oxide synth
22	51	52.6	1433	2 G01945	nitric-oxide synth
23	49	50.5	677	1 RDRG04	NADPH--ferrihemopr
24	49	50.5	677	2 A60557	NADPH--ferrihemopr
25	49	50.5	678	1 RDRTO4	NADPH--ferrihemopr
26	49	50.5	678	2 S27158	NADPH--ferrihemopr
27	48	49.5	671	2 A56592	NADPH--ferrihemopr
28	46	47.4	693	1 S38427	NADPH--ferrihemopr
29	45	46.4	366	2 T31933	hypothetical prote

probable membrane  
hypothetical prote  
transcription/repa  
oligopeptide ABC t  
conserved hypothet  
probable dTDP-gluc  
cuticle protein cu  
hypothetical prote  
hypothetical prote  
ribonucleoside-dip  
hypothetical prote  
hypothetical prote  
probable regulator  
NADPH--ferrihemopr  
hypothetical prote  
peptidase PAB1418

ALIGNMENTS

RESULT 1  
A49676  
nitric-oxide synthase (EC 1.14.13.39), inducible - human  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 20-Jun-2000  
C:Accession: A49676; JX0345; G01947; I38933; S47566; A47475  
R:Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; Hall, V.S.;  
Proc. Natl. Acad. Sci. U.S.A. 90, 11419-11423, 1993  
A:Title: Cloning, characterization, and expression of a cDNA encoding an inducible ni  
A:Reference number: A49676; MUID:94068614  
A:Accession: A49676  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1153 <RES>  
A:Cross-references: EMBL:X73029; NID:g441452; PIDN:CAA51512.1; PID:g441453  
R:Hokari, A.; Zeniya, M.; Esumi, H.  
J. Biochem. 116, 575-581, 1994  
A:Title: Cloning and functional expression of human inducible nitric oxide synthase (  
A:Reference number: JX0345; MUID:95155267  
A:Accession: JX0345  
A:Molecule type: mRNA  
A:Residues: 1-607, 'L', 609-1153 <HOK>  
A:Cross-references: DBJ:D26525; NID:g559326; PIDN:BAA05531.1; PID:g1228940  
R:Park, C.; Park, R.; Krishna, G.  
submitted to the EMBL Data Library, July 1995  
A:Reference number: G08912  
A:Accession: G01947  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-607, 'L', 609-1153 <PAR>  
A:Cross-references: EMBL:U31511; NID:g951320; PIDN:AAB43041.1; PID:g951321  
R:Guo, F.H.; De Raave, H.R.; Rice, T.W.; Stuehr, D.J.; Thunnissen, F.B.; Erzurum, S.C  
Proc. Natl. Acad. Sci. U.S.A. 92, 7809-7813, 1995  
A:Title: Continuous nitric oxide synthesis by inducible nitric oxide synthase in norm  
A:Reference number: I38933; MUID:95372368  
A:Accession: I38933  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-675, 'I', 677-932, 'G', 934-965, 'A', 967-1153 <RE2>  
A:Cross-references: EMBL:U20141; NID:g687680; PIDN:AAB60366.1; PID:g687681  
R:Maier, R.; Bilbe, G.; Rediske, J.; Lotz, M.  
Biochim. Biophys. Acta 1208, 145-150, 1994  
A:Title: Inducible nitric oxide synthase from human articular chondrocytes: cDNA clon  
A:Reference number: S47566; MUID:94368816  
A:Accession: S47566  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-22, 'G', 24-153, 'L', 155-176, 'V', 178-799, 'A', 801-912, 'P', 914-1153 <NAI>  
A:Cross-references: EMBL:U05810; NID:g452487; PIDN:AAA56666.1; PID:g452488  
R:Geller, D.A.; Lowenstein, C.J.; Shapiro, R.A.; Nussler, A.K.; Di Silvio, M.; Wang,  
Proc. Natl. Acad. Sci. U.S.A. 90, 3491-3495, 1993

A:Title: Molecular cloning and expression of inducible nitric oxide synthase from human  
A:Reference number: A47475; MUID:93234523  
A:Accession: A47475  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-422, 'I', 424-804, 'D', 806-830, 'SP', 833-932, 'G', 934-965, 'A', 967-986, 'V', 988-1147, 'L', 1149-1172, 'L', 1174-1199, 'L', 1201-1228, 'L', 1230-1257, 'L', 1259-1286, 'L', 1288-1315, 'L', 1317-1344, 'L', 1346-1373, 'L', 1375-1402, 'L', 1404-1431, 'L', 1433-1460, 'L', 1462-1489, 'L', 1491-1518, 'L', 1520-1547, 'L', 1549-1576, 'L', 1578-1605, 'L', 1607-1634, 'L', 1636-1663, 'L', 1665-1692, 'L', 1694-1721, 'L', 1723-1750, 'L', 1752-1779, 'L', 1781-1808, 'L', 1810-1837, 'L', 1839-1866, 'L', 1868-1895, 'L', 1897-1924, 'L', 1926-1953, 'L', 1955-1982, 'L', 1984-2011, 'L', 2013-2040, 'L', 2042-2069, 'L', 2071-2098, 'L', 2100-2127, 'L', 2129-2156, 'L', 2158-2185, 'L', 2187-2214, 'L', 2216-2243, 'L', 2245-2272, 'L', 2274-2301, 'L', 2303-2330, 'L', 2332-2359, 'L', 2361-2388, 'L', 2390-2417, 'L', 2419-2446, 'L', 2448-2475, 'L', 2477-2504, 'L', 2506-2533, 'L', 2535-2562, 'L', 2564-2591, 'L', 2593-2620, 'L', 2622-2649, 'L', 2651-2678, 'L', 2680-2707, 'L', 2709-2736, 'L', 2738-2765, 'L', 2767-2794, 'L', 2796-2823, 'L', 2825-2852, 'L', 2854-2881, 'L', 2883-2910, 'L', 2912-2939, 'L', 2941-2968, 'L', 2970-2997, 'L', 2999-3026, 'L', 3028-3055, 'L', 3057-3084, 'L', 3086-3113, 'L', 3115-3142, 'L', 3144-3171, 'L', 3173-3200, 'L', 3202-3229, 'L', 3231-3258, 'L', 3260-3287, 'L', 3289-3316, 'L', 3318-3345, 'L', 3347-3374, 'L', 3376-3403, 'L', 3405-3432, 'L', 3434-3461, 'L', 3463-3490, 'L', 3492-3519, 'L', 3521-3548, 'L', 3550-3577, 'L', 3579-3606, 'L', 3608-3635, 'L', 3637-3664, 'L', 3666-3693, 'L', 3695-3722, 'L', 3724-3751, 'L', 3753-3780, 'L', 3782-3809, 'L', 3811-3838, 'L', 3840-3867, 'L', 3869-3896, 'L', 3898-3925, 'L', 3927-3954, 'L', 3956-3983, 'L', 3985-4012, 'L', 4014-4041, 'L', 4043-4070, 'L', 4072-4099, 'L', 4101-4128, 'L', 4130-4157, 'L', 4159-4186, 'L', 4188-4215, 'L', 4217-4244, 'L', 4246-4273, 'L', 4275-4302, 'L', 4304-4331, 'L', 4333-4360, 'L', 4362-4389, 'L', 4391-4418, 'L', 4420-4447, 'L', 4449-4476, 'L', 4478-4505, 'L', 4507-4534, 'L', 4536-4563, 'L', 4565-4592, 'L', 4594-4621, 'L', 4623-4650, 'L', 4652-4679, 'L', 4681-4708, 'L', 4710-4737, 'L', 4739-4766, 'L', 4768-4795, 'L', 4797-4824, 'L', 4826-4853, 'L', 4855-4882, 'L', 4884-4911, 'L', 4913-4940, 'L', 4942-4969, 'L', 4971-4998, 'L', 5000-5027, 'L', 5029-5056, 'L', 5058-5085, 'L', 5087-5114, 'L', 5116-5143, 'L', 5145-5172, 'L', 5174-5201, 'L', 5203-5230, 'L', 5232-5259, 'L', 5261-5288, 'L', 5290-5317, 'L', 5319-5346, 'L', 5348-5375, 'L', 5377-5404, 'L', 5406-5433, 'L', 5435-5462, 'L', 5464-5491, 'L', 5493-5520, 'L', 5522-5549, 'L', 5551-5578, 'L', 5580-5607, 'L', 5609-5636, 'L', 5638-5665, 'L', 5667-5694, 'L', 5696-5723, 'L', 5725-5752, 'L', 5754-5781, 'L', 5783-5810, 'L', 5812-5839, 'L', 5841-5868, 'L', 5870-5897, 'L', 5899-5926, 'L', 5928-5955, 'L', 5957-5984, 'L', 5986-6013, 'L', 6015-6042, 'L', 6044-6071, 'L', 6073-6100, 'L', 6102-6129, 'L', 6131-6158, 'L', 6160-6187, 'L', 6189-6216, 'L', 6218-6245, 'L', 6247-6274, 'L', 6276-6303, 'L', 6305-6332, 'L', 6334-6361, 'L', 6363-6390, 'L', 6392-6419, 'L', 6421-6448, 'L', 6450-6477, 'L', 6479-6506, 'L', 6508-6535, 'L', 6537-6564, 'L', 6566-6593, 'L', 6595-6622, 'L', 6624-6651, 'L', 6653-6680, 'L', 6682-6709, 'L', 6711-6738, 'L', 6740-6767, 'L', 6769-6796, 'L', 6798-6825, 'L', 6827-6854, 'L', 6856-6883, 'L', 6885-6912, 'L', 6914-6941, 'L', 6943-6970, 'L', 6972-6999, 'L', 7001-7028, 'L', 7030-7057, 'L', 7059-7086, 'L', 7088-7115, 'L', 7117-7144, 'L', 7146-7173, 'L', 7175-7202, 'L', 7204-7231, 'L', 7233-7260, 'L', 7262-7289, 'L', 7291-7318, 'L', 7320-7347, 'L', 7349-7376, 'L', 7378-7405, 'L', 7407-7434, 'L', 7436-7463, 'L', 7465-7492, 'L', 7494-7521, 'L', 7523-7550, 'L', 7552-7579, 'L', 7581-7608, 'L', 7610-7637, 'L', 7639-7666, 'L', 7668-7695, 'L', 7697-7724, 'L', 7726-7753, 'L', 7755-7782, 'L', 7784-7811, 'L', 7813-7840, 'L', 7842-7869, 'L', 7871-7898, 'L', 7900-7927, 'L', 7929-7956, 'L', 7958-7985, 'L', 7987-8014, 'L', 8016-8043, 'L', 8045-8072, 'L', 8074-8101, 'L', 8103-8130, 'L', 8132-8159, 'L', 8161-8188, 'L', 8190-8217, 'L', 8219-8246, 'L', 8248-8275, 'L', 8277-8304, 'L', 8306-8333, 'L', 8335-8362, 'L', 8364-8391, 'L', 8393-8420, 'L', 8422-8449, 'L', 8451-8478, 'L', 8480-8507, 'L', 8509-8536, 'L', 8538-8565, 'L', 8567-8594, 'L', 8596-8623, 'L', 8625-8652, 'L', 8654-8681, 'L', 8683-8710, 'L', 8712-8739, 'L', 8741-8768, 'L', 8770-8797, 'L', 8799-8826, 'L', 8828-8855, 'L', 8857-8884, 'L', 8886-8913, 'L', 8915-8942, 'L', 8944-8971, 'L', 8973-9000, 'L', 9002-9029, 'L', 9031-9058, 'L', 9060-9087, 'L', 9089-9116, 'L', 9118-9145, 'L', 9147-9174, 'L', 9176-9203, 'L', 9205-9232, 'L', 9234-9261, 'L', 9263-9290, 'L', 9292-9319, 'L', 9321-9348, 'L', 9350-9377, 'L', 9379-9406, 'L', 9408-9435, 'L', 9437-9464, 'L', 9466-9493, 'L', 9495-9522, 'L', 9524-9551, 'L', 9553-9580, 'L', 9582-9609, 'L', 9611-9638, 'L', 9640-9667, 'L', 9669-9696, 'L', 9698-9725, 'L', 9727-9754, 'L', 9756-9783, 'L', 9785-9812, 'L', 9814-9841, 'L', 9843-9870, 'L', 9872-9899, 'L', 9901-9928, 'L', 9930-9957, 'L', 9959-9986, 'L', 9988-10015, 'L', 10017-10044, 'L', 10046-10073, 'L', 10075-10102, 'L', 10104-10131, 'L', 10133-10160, 'L', 10162-10189, 'L', 10191-10218, 'L', 10220-10247, 'L', 10249-10276, 'L', 10278-10305, 'L', 10307-10334, 'L', 10336-10363, 'L', 10365-10392, 'L', 10394-10421, 'L', 10423-10450, 'L', 10452-10479, 'L', 10481-10508, 'L', 10510-10537, 'L', 10539-10566, 'L', 10568-10595, 'L', 10597-10624, 'L', 10626-10653, 'L', 10655-10682, 'L', 10684-10711, 'L', 10713-10740, 'L', 10742-10769, 'L', 10771-10798, 'L', 10800-10827, 'L', 10829-10856, 'L', 10858-10885, 'L', 10887-10914, 'L', 10916-10943, 'L', 10945-10972, 'L', 10974-11001, 'L', 11003-11030, 'L', 11032-11059, 'L', 11061-11088, 'L', 11090-11117, 'L', 11119-11146, 'L', 11148-11175, 'L', 11177-11204, 'L', 11206-11233, 'L', 11235-11262, 'L', 11264-11291, 'L', 11293-11320, 'L', 11322-11349, 'L', 11351-11378, 'L', 11380-11407, 'L', 11409-11436, 'L', 11438-11465, 'L', 11467-11494, 'L', 11496-11523, 'L', 11525-11552, 'L', 11554-11581, 'L', 11583-11610, 'L', 11612-11639, 'L', 11641-11668, 'L', 11670-11697, 'L', 11699-11726, 'L', 11728-11755, 'L', 11757-11784, 'L', 11786-11813, 'L', 11815-11842, 'L', 11844-11871, 'L', 11873-11900, 'L', 11902-11929, 'L', 11931-11958, 'L', 11960-11987, 'L', 11989-12016, 'L', 12018-12045, 'L', 12047-12074, 'L', 12076-12103, 'L', 12105-12132, 'L', 12134-12161, 'L', 12163-12190, 'L', 12192-12219, 'L', 12221-12248, 'L', 12250-12277, 'L', 12279-12306, 'L', 12308-12335, 'L', 12337-12364, 'L', 12366-12393, 'L', 12395-12422, 'L', 12424-12451, 'L', 12453-12480, 'L', 12482-12509, 'L', 12511-12538, 'L', 12540-12567, 'L', 12569-12596, 'L', 12598-12625, 'L', 12627-12654, 'L', 12656-12683, 'L', 12685-12712, 'L', 12714-12741, 'L', 12743-12770, 'L', 12772-12799, 'L', 12801-12828, 'L', 12830-12857, 'L', 12859-12886, 'L', 12888-12915, 'L', 12917-12944, 'L', 12946-12973, 'L', 12975-13002, 'L', 13004-13031, 'L', 13033-13060, 'L', 13062-13089, 'L', 13091-13118, 'L', 13120-13147, 'L', 13149-13176, 'L', 13178-13205, 'L', 13207-13234, 'L', 13236-13263, 'L', 13265-13292, 'L', 13294-13321, 'L', 13323-13350, 'L', 13352-13379, 'L', 13381-13408, 'L', 13410-13437, 'L', 13439-13466, 'L', 13468-13495, 'L', 13497-13524, 'L', 13526-13553, 'L', 13555-13582, 'L', 13584-13611, 'L', 13613-13640, 'L', 13642-13669, 'L', 13671-13698, 'L', 13700-13727, 'L', 13729-13756, 'L', 13758-13785, 'L', 13787-13814, 'L', 13816-13843, 'L', 13845-13872, 'L', 13874-13901, 'L', 13903-13930, 'L', 13932-13959, 'L', 13961-13988, 'L', 13990-14017, 'L', 14019-14046, 'L', 14048-14075, 'L', 14077-14104, 'L', 14106-14133, 'L', 14135-14162, 'L', 14164-14191, 'L', 14193-14220, 'L', 14222-14249, 'L', 14251-14278, 'L', 14280-14307, 'L', 14309-14336, 'L', 14338-14365, 'L', 14367-14394, 'L', 14396-14423, 'L', 14425-14452, 'L', 14454-14481, 'L', 14483-14510, 'L', 14512-14539, 'L', 14541-14568, 'L', 14570-14597, 'L', 14599-14626, 'L', 14628-14655, 'L', 14657-14684, 'L', 14686-14713, 'L', 14715-14742, 'L', 14744-14771, 'L', 14773-14800, 'L', 14802-14829, 'L', 14831-14858, 'L', 14860-14887, 'L', 14889-14916, 'L', 14918-14945, 'L', 14947-14974, 'L', 14976-15003, 'L', 15005-15032, 'L', 15034-15061, 'L', 15063-15090, 'L', 15092-15119, 'L', 15121-15148, 'L', 15150-15177, 'L', 15179-15206, 'L', 15208-15235, 'L', 15237-15264, 'L', 15266-15293, 'L', 15295-15322, 'L', 15324-15351, 'L', 15353-15380, 'L', 15382-15409, 'L', 15411-15438, 'L', 15440-15467, 'L', 15469-15496, 'L', 15498-15525, 'L', 15527-15554, 'L', 15556-15583, 'L', 15585-15612, 'L', 15614-15641, 'L', 15643-15670, 'L', 15672-15699, 'L', 15701-15728, 'L', 15730-15757, 'L', 15759-15786, 'L', 15788-15815, 'L', 15817-15844, 'L', 15846-15873, 'L', 15875-15902, 'L', 15904-15931, 'L', 15933-15960, 'L', 15962-15989, 'L', 15991-16018, 'L', 16020-16047, 'L', 16049-16076, 'L', 16078-16105, 'L', 16107-16134, 'L', 16136-16163, 'L', 16165-16192, 'L', 16194-16221, 'L', 16223-16250, 'L', 16252-16279, 'L', 16281-16308, 'L', 16310-16337, 'L', 16339-16366, 'L', 16368-16395, 'L', 16397-16424, 'L', 16426-16453, 'L', 16455-16482, 'L', 16484-16511, 'L', 16513-16540, 'L', 16542-16569, 'L', 16571-16598, 'L', 16600-16627, 'L', 16629-16656, 'L', 16658-16685, 'L', 16687-16714, 'L', 16716-16743, 'L', 16745-16772, 'L', 16774-16801, 'L', 16803-16830, 'L', 16832-16859, 'L', 16861-16888, 'L', 16890-16917, 'L', 16919-16946, 'L', 16948-16975, 'L', 16977-17004, 'L', 17006-17033, 'L', 17035-17062, 'L', 17064-17091, 'L', 17093-17120, 'L', 17122-17149, 'L', 17151-17178, 'L', 17180-17207, 'L', 17209-17236, 'L', 17238-17265, 'L', 17267-17294, 'L', 17296-17323, 'L', 17325-17352, 'L', 17354-17381, 'L', 17383-17410, 'L', 17412-17439, 'L', 17441-17468, 'L', 17470-17497, 'L', 17499-17526, 'L', 17528-17555, 'L', 17557-17584, 'L', 17586-17613, 'L', 17615-17642, 'L', 17644-17671, 'L', 17673-17700, 'L', 17702-17729, 'L', 17731-17758, 'L', 17760-17787, 'L', 17789-17816, 'L', 17818-17845, 'L', 17847-17874, 'L', 17876-17903, 'L', 17905-17932, 'L', 17934-17961, 'L', 17963-17990, 'L', 17992-18019, 'L', 18021-18048, 'L', 18050-18077, 'L', 18079-18106, 'L', 18108-18135, 'L', 18137-18164, 'L', 18166-18193, 'L', 18195-18222, 'L', 18224-18251, 'L', 18253-18280, 'L', 18282-18309, 'L', 18311-18338, 'L', 18340-18367, 'L', 18369-18396, 'L', 18398-18425, 'L', 18427-18454, 'L', 18456-18483, 'L', 18485-18512, 'L', 18514-18541, 'L', 18543-18570, 'L', 18572-18599, 'L', 18601-18628, 'L', 18630-18657, 'L', 18659-18686, 'L', 18688-18715, 'L', 18717-18744, 'L', 18746-18773, 'L', 18775-18802, 'L', 18804-18831, 'L', 18833-18860, 'L', 18862-18889, 'L', 18891-18918, 'L', 18920-18947, 'L', 18949-18976, 'L', 18978-19005, 'L', 19007-19034, 'L', 19036-19063, 'L', 19065-19092, 'L', 19094-19121, 'L', 19123-19150, 'L', 19152-19179, 'L', 19181-19208, 'L', 19210-19237, 'L', 19239-19266, 'L', 19268-19295, 'L', 19297-19324, 'L', 19326-19353, 'L', 19355-19382, 'L', 19384-19411, 'L', 19413-19440, 'L', 19442-19469, 'L', 19471-19498, 'L', 19500-19527, 'L', 19529-19556, 'L', 19558-19585, 'L', 19587-19614, 'L', 19616-19643, 'L', 19645-19672, 'L', 19674-19701, 'L', 19703-19730, 'L', 19732-19759, 'L', 19761-19788, 'L', 19790-19817, 'L', 19819-19846, 'L', 19848-19875, 'L', 19877-19904, 'L', 19906-19933, 'L', 19935-19962, 'L', 19964-19991, 'L', 19993-20020, 'L', 20022-20049, 'L', 20051-20078, 'L', 20080-20107, 'L', 20109-20136, 'L', 20138-20165, 'L', 20167-20194, 'L', 20196-20223, 'L', 20225-20252, 'L', 20254-20281, 'L', 20283-20310, 'L', 20312-20339, 'L', 20341-20368, 'L', 20370-20397, 'L', 20399-20426, 'L', 20428-20455, 'L', 20457-20484, 'L', 20486-20513, 'L', 20515-20542, 'L', 20544-20571, 'L', 20573-20600, 'L', 20602-20629, 'L', 20631-20658, 'L', 20660-20687, 'L', 20689-20716, 'L', 20718-20745, 'L', 20747-20774, 'L', 20776-20803, 'L', 20805-20832, 'L', 20834-20861, 'L', 20863-20890, 'L', 20892-20919, 'L', 20921-20948, 'L', 20950-20977, 'L', 20979-21006, 'L', 21008-21035, 'L', 21037-21064, 'L', 21066-21093, 'L', 21095-21122, 'L', 21124-21151, 'L', 21153-21180, 'L', 21182-21209, 'L', 21211-21238, 'L', 21240-21267, 'L', 21269-21296, 'L', 21298-21325, 'L', 21327-21354, 'L', 21356-21383, 'L', 21385-21412, 'L', 21414-21441, 'L', 21443-21470, 'L', 21472-21499, 'L', 21501-21528, 'L', 21530-21557, 'L', 21559-21586, 'L', 21588-21615, 'L', 21617-21644, 'L', 21646-21673, 'L', 21675-21702, 'L', 21704-21731, 'L', 21733-21760, 'L', 21762-21789, 'L', 21791-21818, 'L', 21820-21847, 'L', 21849-21876, 'L', 21878-21905, 'L', 21907-21934, 'L', 21936-21963, 'L', 21965-21992, 'L', 21994-22021, 'L', 22023-22050, 'L', 22052-22079, 'L', 22081-22108, 'L', 22110-22137, 'L', 22139-22166, 'L', 22168-22195, 'L', 22197-22224, 'L', 22226-22253, 'L', 22255-22282, 'L', 22284-22311, 'L', 22313-22340, 'L', 22342-22369, 'L', 22371-22398, 'L', 22400-22427, 'L', 22429-22456, 'L', 22458-22485, 'L', 22487-22514, 'L', 22516-22543, 'L', 22545-22572, 'L', 22574-22601, 'L', 22603-22630, 'L', 22632-22659, 'L', 22661-22688, 'L', 22690-22717, 'L', 22719-22746, 'L', 22748-22775, 'L', 22777-22804, 'L', 22806-22833, 'L', 22835-22862, 'L', 22864-22891, 'L', 22893-22920, 'L', 22922-22949, 'L', 22951-22978, 'L', 22980-23007, 'L', 23009-23036, 'L', 23038-23065, 'L', 23067-23094, 'L', 23096-23123, 'L', 23125-23152, 'L', 23154-23181, 'L', 23183-23210, 'L', 23212-23239, 'L', 23241-23268, 'L', 23270-23297, 'L', 23299-23326, 'L', 23328-23355, 'L', 23357-23384, 'L', 23386-23413, 'L', 23415-23442, 'L', 23444-23471, 'L', 23473-23500, 'L', 23502-23529, 'L', 23531-23558, 'L', 23560-23587, 'L', 23589-23616, 'L', 23618-23645, 'L', 23647-23674, 'L', 23676-23703, 'L', 23705-23732, 'L', 23734-23761, 'L', 23763-23790, 'L', 23792-23819, 'L', 23821-23848, 'L', 23850-23877, 'L', 23879-23906, 'L', 23908-23935, 'L', 23937-23964, 'L', 23966-23993, 'L', 23995-24022, 'L', 24024-24051, 'L', 24053-24080, 'L', 24082-24



A:Reference number: S38253; MUID:94039059

A:Accession: S38253

A:Molecule type: mRNA

A:Residues: 1-1147 <ADA>

A:Cross-references: GB:D12520; NID:g391858; PIDN:BAA02090.1; PID:g391859

A:Experimental source: liver

R:Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.

Biochem. Biophys. Res. Commun. 191, 767-774, 1993

A:Title: Hepatocytes and macrophages express an identical cytokine inducible nitric oxide

A:Reference number: JN0457; MUID:93221515

A:Accession: JN0457

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-41, 'SS', 44-103, 105-190, 'Q', 192-213, 'R', 215-247, 'T', 249-263, 'I', 265-373, 'IE

'S', 896-1000, 'LG', 1003-1015, 'RR', 1018-1026, 'EQ', 1029-1147 <WOO>

A:Cross-references: PIDN:AAB26037.1

A:Experimental source: liver

C:Genetics:

A:Gene: NOS

C:Function:

C:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reduc

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal

F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>

F:538-674/Domain: flavodoxin homology <FLX>

F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 83.5%; Score 81; DB 1; Length 1147;

Best Local Similarity 77.8%; Pred. No. 1.1e-05;

Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RMTLVFSGRRPDEDHIYQ 18

||||||| | | | | |

Db 1006 RMTLVFGCRHPEEDHLYQ 1023

RESULT 6

153165

nitric-oxide synthase (EC 1.14.13.39) [similarity] - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 05-May-2000

C:Accession: I53165

R:Karlsen, A.E.; Andersen, H.U.; Vissing, H.; Larsen, P.M.; Fey, S.J.; Cuartero, B.G.; M

Diabetes 44, 753-758, 1995

A:Title: Cloning and expression of cytokine-inducible nitric oxide synthase cDNA from ra

A:Reference number: I53165; MUID:95309542

A:Accession: I53165

A:Status: translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-1147 <RES>

A:Cross-references: EMBL:U26686; NID:g886072; PIDN:AAA85861.1; PID:g886073

C:Genetics:

A:Gene: NOS2

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reduc

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal

F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>

F:538-674/Domain: flavodoxin homology <FLX>

F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 83.5%; Score 81; DB 1; Length 1147;

Best Local Similarity 77.8%; Pred. No. 1.1e-05;

Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RMTLVFSGRRPDEDHIYQ 18

||||||| | | | | |

Db 1006 RMTLVFGCRHPEEDHLYQ 1023

RESULT 7

JC5029

nitric-oxide synthase (EC 1.14.13.39) U - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 04-Mar-2000

C:Accession: JC5029

R:Tsutsunishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa

Biol. Pharm. Bull. 19, 1374-1376, 1996

A:Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, an

A:Reference number: JC5027; MUID:97070590

A:Accession: JC5029

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1147 <TSU>

A:Experimental source: uterus

C:Comment: This protein synthesizes nitric oxide from L-arginine.

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein re

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me

F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>

F:538-674/Domain: flavodoxin homology <FLX>

F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 83.5%; Score 81; DB 2; Length 1147;

Best Local Similarity 77.8%; Pred. No. 1.1e-05;

Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RMTLVFSGRRPDEDHIYQ 18

||||||| | | | | |

Db 1006 RMTLVFGCRHPEEDHLYQ 1023

RESULT 8

S65440

nitric-oxide synthase (EC 1.14.13.39) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 04-Mar-2000

C:Accession: S65440

R:Iwashina, M.; Hirata, Y.; Imai, T.; Sato, K.; Marumo, F.

Eur. J. Biochem. 237, 668-673, 1996

A:Title: Molecular cloning of endothelial, inducible nitric oxide synthase gene from

A:Reference number: S65440; MUID:96235231

A:Accession: S65440

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-1147 <IWA>

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein re

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me

F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>

F:538-674/Domain: flavodoxin homology <FLX>

F:599-618/Region: biopterin binding

F:620-647/Region: FMN binding #status predicted

F:764-775/Region: FAD binding #status predicted

F:901-910/Region: FAD binding #status predicted

F:975-993/Region: NADPH binding #status predicted

F:1074-1087/Region: NADPH binding #status predicted

F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match

Best Local Similarity 77.8%; Score 81; DB 2; Length 1147;

Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RMTLVFSGRRPDEDHIYQ 18

||||||| | | | | |

Db 1006 RMTLVFGCRHPEEDHLYQ 1023

RESULT 9

A43271

nitric-oxide synthase (EC 1.14.13.39), calmodulin-independent - mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Mar-2000

C:Accession: A43271; A42166; JN0458; A46186

R:Xie, Q.; Cho, H.J.; Calaycay, J.; Mumford, R.A.; Swiderek, K.M.; Lee, T.D.; Ding, A

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrirhemoprotein re  
C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me  
F:191-199/Domain: heme-binding #status predicted <HMB>  
F:536-1124/Domain: NADPH--ferrirhemoprotein reductase homology <FEH>  
F:538-674/Domain: flavodoxin homology <FLX>  
F:620-647/Domain: FMN binding #status predicted <FMN>  
F:764-775;899-910/Domain: FAD binding #status predicted <FAD>  
F:975-993;1054-1067/Domain: NADP binding #status predicted <NDP>  
F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 71.1%; Score 69; DB 2; Length 1147;  
Best Local Similarity 72.2%; Pred. No. 0.0013;  
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RMTLVFGSRPDEDHIYQ 18  
||||||| | ||| ||  
Db 1006 RMTLVFGCRHREDHLQY 1023

RESULT 11  
JC5028  
nitric-oxide synthase (EC 1.14.13.39) L - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 04-Mar-2000  
C:Accession: JC5028  
R:Tsutsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa  
Biol. Pharm. Bull. 19, 1374-1376, 1996  
A:Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, an  
A:Reference number: JC5027; MUID:97070590  
A:Accession: JC5028  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1147 <TSU>  
A:Experimental source: lung  
C:Comment: This protein synthesizes nitric oxide from L-arginine.  
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrirhemoprotein re  
C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me  
F:536-1124/Domain: NADPH--ferrirhemoprotein reductase homology <FEH>  
F:538-674/Domain: flavodoxin homology <FLX>  
F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 71.1%; Score 69; DB 2; Length 1147;  
Best Local Similarity 72.2%; Pred. No. 0.0013;  
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RMTLVFGSRPDEDHIYQ 18  
||||||| | ||| ||  
Db 1006 RMTLVFGCRHREDHLQY 1023

RESULT 12  
I38067  
nitric-oxide synthase (EC 1.14.13.39) Irb - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 11-Jun-1999  
C:Accession: I38067  
R:Blöchl, K.D.; Wolfgram, J.R.; Brown, D.M.; Roberts, J.D.  
Genomics 27, 526-530, 1995  
A:Title: Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, and  
A:Reference number: A57622; MUID:96047340  
A:Accession: I38067  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: DNA  
A:Residues: 1-49 <RES>  
A:Cross-references: EMBL:U18333; NID:g1041684; PIDN:AAC50233.1; PID:g1041687  
C:Genetics:  
A:Gene: GDB:NOS2B  
A:Cross-references: GDB:547926; OMIM:600719  
A:Map position: 17p13.1-17q25  
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrirhemoprotein re  
C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me

Query Match 68.0%; Score 66; DB 2; Length 49;  
 Best Local Similarity 72.2%; Pred. No. 0.00013;  
 Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RMTLVFGSRRPDEDEHIYQ 18  
 ||| || | | | | | | | |  
 Db 5 RMTVPVFCRSPNEDHIYQ 22

## RESULT 13

I39204

nitric-oxide synthase (EC 1.14.13.39) 2C - human (fragment)

N;Alternate names: nitric oxide synthase II

C:Species: Homo sapiens (man)

C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 11-Jun-1999

C:Accession: I39204

R:Blach, K.D.; Wolfram, J.R.; Brown, D.M.; Roberts, J.D.

Genomics 27, 526-530, 1995

A:Title: Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, and NOS2C)

A:Reference number: A57622; MUID:96047340

A:Accession: I39204

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-69 <RES>

A:Cross-references: EMBL:U18335; NID:g1050946; PIDN:AAC50245.1; PID:g1050948

C:Genetics:

A:Gene: GDB:NOS2C

A:Cross-references: GDB:547943; OMIM:600720

A:Map position: 17p13.1-17q25

A:Introns: 33/1

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrirhemoprotein reductase

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; NADP;

## Query Match

Best Local Similarity 60.8%; Score 59; DB 2; Length 69;

Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RMTLVFGSRRPDEDEHIYQ 18  
 ||| || | | | | | | | |  
 Db 38 RRTLVFWCRRPDEDRHYR 55

## RESULT 14

A69975

cytochrome P450 / NADPH--ferrirhemoprotein reductase yrhJ [similarity] - Bacillus subtilis

N;Contents: NADPH--ferrirhemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (EC 1.10.3.1)

C:Species: Bacillus subtilis

C:Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 28-Jul-2000

C:Accession: A69975

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berto

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A.; Mathers, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue

y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serod

akeuchi, M.; Takakoshi, A.; Tanaka, T.; Terpstra, P.; Toononi, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Zumbstein, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033

A:Accession: A69975

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1054 <RES>

A:Cross-references: GB:Z99117; GB:AL009126; NID:g2634966; PID:g2635162

A:Experimental source: strain 168

C:Gene: yrhJ

C:Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin

C:Keywords: chromoprotein; flavoprotein; heme; iron; metalloprotein; monooxygenase; o

F:486-1050/Domain: NADPH--ferrirhemoprotein reductase homology <FEH>

F:488-625/Domain: flavodoxin homology <FLX>

F:403/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 53.6%; Score 52; DB 1; Length 1054;

Best Local Similarity 60.0%; Pred. No. 1;

Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LVFGSRRPDEDEHIYQ 18  
 ||| || | | | | | | | |  
 Db 937 LYFGCRRPDHDLRYR 951

## RESULT 15

I51917

nitric-oxide synthase (EC 1.14.13.39) 3 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 11-Jun-1999

C:Accession: I51917

R:Kawai, N.; Bloch, D.B.; Philippov, G.; Rabkina, D.; Suen, H.C.; Losty, P.D.; Janssen

Am. J. Physiol. 268, L589-L595, 1995

A:Title: Constitutive endothelial nitric oxide synthase gene expression is regulated

A:Reference number: I51917; MUID:95250990

A:Accession: I51917

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-63 <RES>

A:Cross-references: EMBL:U18336; NID:g806761; PIDN:AAC52188.1; PID:g806762

C:Genetics:

A:Gene: NOS3

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrirhemoprotein re

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; NA

## Query Match

Best Local Similarity 52.6%; Score 51; DB 2; Length 63;

Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 MTLVFGSRRPDEDEHIYQ 18  
 ||| || | | | | | | | |  
 Db 24 MTLVFGCRCSQLDHLRYR 40

Search completed: September 10, 2001, 14:01:15

Job time: 214 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:00:25 ; Search time 67.08 Seconds  
(without alignments)  
16.268 Million cell updates/sec

Title: US-08-833-506c-31

Perfect score: 97

Sequence: 1 RMTLVFGSRPDEHHIQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

1:	/SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2:	/SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3:	/SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4:	/SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5:	/SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6:	/SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7:	/SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8:	/SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9:	/SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10:	/SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11:	/SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12:	/SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13:	/SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14:	/SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15:	/SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16:	/SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17:	/SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18:	/SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19:	/SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20:	/SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21:	/SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22:	/SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	97	100.0	18	AAW81252	Human iNOS peptide
2	97	100.0	18	AAW81279	Human iNOS peptide
3	97	100.0	18	AAW81210	Human iNOS peptide
4	92	94.8	18	AAW81192	Human iNOS (1009-1
5	92	94.8	1146	20 AAW96322	Inducible nitric o
6	92	94.8	1153	15 AAR55764	Sequence encoded b
7	92	94.8	1153	15 AAR63206	Nitric-oxide-synth
8	92	94.8	1153	17 AAR88464	Hepatocyte inducib
9	92	94.8	1153	19 AAW36113	Human inducible ni
10	92	94.8	1153	22 AAB31724	Amino acid sequenc
11	92	94.8	1153	22 AAB66724	Human inducible ni

12	82	84.5	15	19	AAW81255	Human iNOS peptide
13	82	84.5	15	19	AAW81312	Human iNOS peptide
14	81	83.5	15	19	AAW81259	Human iNOS peptide
15	81	83.5	15	19	AAW81316	Human iNOS peptide
16	81	83.5	1147	17	AAW02571	Rat inducible nitr
17	77	79.4	18	19	AAW81194	Murine iNOS (1002-
18	77	79.4	1144	16	AAW77360	Inducible nitrogen
19	77	79.4	1144	19	AAW51246	Inducible nitric o
20	71	73.2	18	19	AAW81193	Ray iNOS (1006-102
21	68	70.1	12	19	AAW81256	Human iNOS peptide
22	68	70.1	12	19	AAW81313	Human iNOS peptide
23	58	59.8	17	19	AAW81253	Human eNOS peptide
24	58	59.8	17	19	AAW81325	Human iNOS peptide
25	56	57.7	11	19	AAW81260	Human iNOS peptide
26	56	57.7	11	19	AAW81317	Human iNOS peptide
27	56	57.7	17	19	AAW81254	Human iNOS peptide
28	56	57.7	17	19	AAW81326	Human iNOS peptide
29	53	54.6	9	19	AAW81257	Human iNOS peptide
30	53	54.6	9	19	AAW81314	Human iNOS peptide
31	51	52.6	1048	22	AAW811978	Amino acid sequenc
32	51	52.6	1048	22	AAW811979	Amino acid sequenc
33	51	52.6	1048	22	AAW811980	Amino acid sequenc
34	51	52.6	1048	22	AAW811981	Amino acid sequenc
35	51	52.6	1048	22	AAW811985	B. megaterium cyto
36	51	52.6	1048	22	AAW811986	B. megaterium cyto
37	51	52.6	1049	21	AAW811987	Amino acid sequenc
38	51	52.6	1049	22	AAW811988	Amino acid sequenc
39	51	52.6	1049	22	AAW811989	Bacillus megateriu
40	51	52.6	1085	12	AAW811604	P450 17-alpha/P450
41	51	52.6	1203	14	AAW811668	Human endothelial
42	51	52.6	1203	19	AAW811726	Human endothelial
43	51	52.6	1203	22	AAW811726	Amino acid sequenc
44	51	52.6	1203	22	AAW811726	Human nitric oxide
45	51	52.6	1205	16	AAW811736	Endothelial nitrog

#### ALIGNMENTS

RESULT 1

AAW81252

ID AAW81252 standard; peptide; 18 AA.

XX

AC AAW81252;

XX

DT 30-APR-1999 (first entry)

XX

DE Human iNOS peptide fragment PS-5185.

XX

KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;

KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;

KW myocardial infarction; tissue rejection; transplantation; psoriasis;

KW autoimmune disease; multiple sclerosis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 18

FT /note= "Gln residue amidated".

XX

PN W09845710-A1.

XX

PD 15-OCT-1998.

XX

PF 11-APR-1997; 97WO-US065500.

XX

PR 07-APR-1997; 97US-6667777.

XX

PA (WEBB/) WEBBER R.

XX

PI Webber R;

XX

DR WPI; 1998-594495/50.

XX Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
XX  
PS Example 4; Page 39; 93pp; English.  
XX  
CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathophysiological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
XX invention.  
XX Sequence 18 AA;  
SQ  
Query Match 100.0%; Score 97; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.7e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RMTLVFSGRRPDEDHIYQ 18  
Db 1 rmtlvfsgrrpdedhiyq 18  
|||||  
RESULT 2  
AAW81279  
ID AAW81279 standard; peptide; 18 AA.  
XX  
AC AAW81279;  
XX  
DT 30-APR-1999 (first entry)  
XX  
DE Human iNOS peptide fragment #5.  
XX  
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis.  
XX  
OS Homo sapiens.  
XX  
PN WO9845710-A1.  
XX  
PD 15-OCT-1998.  
XX  
PF 11-APR-1997; 97WO-US06500.  
XX  
PR 07-APR-1997; 97US-6667777.  
XX  
PA (WEBB/) WEBBER R.  
XX  
PI Webber R;  
XX  
DR WO9845710-A1.  
XX  
PD 15-OCT-1998.  
XX  
PF 11-APR-1997; 97WO-US06500.  
XX  
PR 07-APR-1997; 97US-6667777.  
XX  
PA (WEBB/) WEBBER R.  
XX  
PI Webber R;  
XX  
DR WPI; 1998-594495/50.  
XX  
PT Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
XX  
PS Disclosure; Fig 1; 93pp; English.  
XX  
CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and

CC tissues for various pathophysiological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
XX invention.  
XX Sequence 18 AA;  
SQ  
Query Match 100.0%; Score 97; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.7e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RMTLVFSGRRPDEDHIYQ 18  
Db 1 rmtlvfsgrrpdedhiyq 18  
|||||  
RESULT 3  
AAW81210  
ID AAW81210 standard; peptide; 18 AA.  
XX  
AC AAW81210;  
XX  
DT 30-APR-1999 (first entry)  
XX  
DE Human iNOS peptide fragment capable of binding Mab 24B10-2C7.  
XX  
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis; Mab.  
XX  
OS Homo sapiens.  
XX  
PN WO9845710-A1.  
XX  
PD 15-OCT-1998.  
XX  
PF 11-APR-1997; 97WO-US06500.  
XX  
PR 07-APR-1997; 97US-6667777.  
XX  
PA (WEBB/) WEBBER R.  
XX  
PI Webber R;  
XX  
DR WPI; 1998-594495/50.  
XX  
PT Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
XX  
PS Example 3; Page 33; 93pp; English.  
XX  
CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathophysiological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
XX invention.  
XX Sequence 18 AA;  
SQ  
Query Match 100.0%; Score 97; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.7e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMTLVFSGRRPDEDHIYQ 18  
 |||||  
 Db 1 rmtlvfsgrrpdedhiyq 18

RESULT 4  
 AAW81192  
 ID AAW81192 standard; peptide; 18 AA.  
 XX AC  
 XX AC AAW81192;  
 XX AC  
 DT 30-APR-1999 (first entry)  
 XX  
 XX Human iNOS (1009-1026) peptide fragment.  
 DE  
 XX Inducible nitric oxide synthase; iNOS; human; immunoassay; detection;  
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
 KW autoimmune disease; multiple sclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9845710-A1.  
 PN  
 XX 15-OCT-1998.  
 PD  
 XX 11-APR-1997; 97WO-US06500.  
 PF  
 XX 07-APR-1997; 97US-666777.  
 PR  
 XX (WEBB/) WEBBER R.  
 PA  
 XX Webber R;  
 PI  
 XX WPI; 1998-594495/50.  
 DR  
 XX Detection of human inducible nitric oxide synthase - using an  
 PT immunoassay in which a sample is contacted with a specific binding  
 PT entity reactive with human iNOS or mimics.  
 PT  
 XX Disclosure; Page 21; 93pp; English.  
 PS  
 XX This invention describes an immunoassay method where a sample with a  
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
 CC to detect the presence of human iNOS protein in the sample. The method  
 CC can be used for the detection and quantitation of human iNOS in cells and  
 CC tissues for various pathophysiological conditions such as sepsis, septic  
 CC shock, myocardial infarction, rejection of tissue in organs following  
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
 CC represents a peptide fragment from human iNOS which is used in the method  
 CC of the invention.  
 XX  
 XX Sequence 18 AA;

Query Match 94.8%; Score 92; DB 19; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.le-08;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RMTLVFSGRRPDEDHIYQ 18  
 |||||  
 Db 1 rmtlvfsgrrpdedhiyq 18

RESULT 5  
 AAW96322  
 ID AAW96322 standard; Protein; 1146 AA.  
 XX AC  
 XX AAW96322;

XX 28-JUN-1999 (first entry)  
 DT  
 XX Inducible nitric oxide synthase.  
 DE  
 XX Manganese containing superoxide dismutase; MnSOD; IDDM;  
 KW diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell;  
 KW fatty acid; lipotoxic; cytotoxic; cytokine; osteoporosis;  
 KW inflammatory disease; autoimmune disease; neurodegenerative disease.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO9906059-A2.  
 PN  
 XX 11-FEB-1999.  
 PD  
 XX 30-JUL-1998; 98WO-US15781.  
 PF  
 XX 03-MAR-1998; 98US-0055092.  
 PR  
 PR 30-JUL-1997; 97US-0055092.  
 XX  
 XX (BETA-) BETAGENE INC.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Clark SA, Hohmeier H, Koyama K, Lee Y, Newgard CB;  
 XX Ohneda M, Shimabukuro, Thigpen A, Unger RH;  
 PI  
 XX WPI; 1999-153448/13.  
 DR N-PSDB; AAX08434.  
 DR  
 XX Protection of mammalian cells against immunotoxicity or lipotoxicity  
 PT - used for treating, e.g. diabetes, obesity, wasting syndromes,  
 PT osteoporosis, inflammatory diseases, autoimmune diseases or  
 PT neurodegenerative diseases  
 PT  
 XX Disclosure; Page 247-251; 253pp; English.  
 PS  
 XX Inhibition of cytokine mediated immunotoxicity of cells can be  
 CC achieved by blocking free radical production or the accumulation of  
 CC free radicals in that cell. Treatment of insulin dependent diabetes  
 CC mellitus (IDDM) can be achieved by blocking nitric oxide (NO)  
 CC production in a pancreatic beta cell and by providing a composition  
 CC comprising an agent that reduces levels of fatty acids in the cells  
 CC and protects beta-cells of the subject against nitric oxide mediated  
 CC cytotoxicity by introducing into the cell an antioxidant agent.  
 CC The methods can be used for protecting cells against immunotoxicity  
 CC mediated by, e.g. IL-1 beta, IL-1 alpha, gamma IFN, TNF alpha, TNF  
 CC beta, IL-8, IL-2, IL-6, IL-2, IL-3, IL-5, IL-7, IL-9, IL-14, IL-17,  
 CC granulocyte-macrophage colony stimulating factor or monocyte  
 CC chemoattractant protein-1. The methods can be used for the treatment  
 CC of e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity,  
 CC wasting syndromes, short stature, osteoporosis, inflammatory  
 CC diseases, autoimmune diseases, or neurodegenerative diseases.  
 CC  
 XX Sequence 1146 AA;

Query Match 94.8%; Score 92; DB 20; Length 1146;  
 Best Local Similarity 94.4%; Pred. No. 1e-06;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RMTLVFSGRRPDEDHIYQ 18  
 |||||  
 Db 1009 rmtlvfsgrrpdedhiyq 1026

RESULT 6  
 AAR55764  
 ID AAR55764 standard; Protein; 1153 AA.  
 XX AC  
 XX AAR55764;

DT 28-DEC-1994 (first entry)  
 XX Sequence encoded by the cDNA clone for human hepatocyte inducible  
 DE nitric oxide synthase.  
 XX  
 XX Nitric oxide synthase; hepatocyte; hypotensive shock; therapy.  
 XX Homo sapiens.  
 OS  
 XX WO9412645-A.  
 PN  
 XX 09-JUN-1994.  
 PD  
 XX 23-NOV-1993; 93WO-US11401.  
 XX  
 XX 25-NOV-1992; 92US-0981344.  
 PR  
 XX (UYPI-) UNIV PITTSBURGH.  
 PA  
 XX Billiar TR, Geller DA, Nussler AK, Simmons RL;  
 PI  
 XX WPI: 1994-200273/24.  
 DR  
 XX N-PSDB; AAQ66914.  
 DR  
 XX cDNA clone encoding human inducible nitric oxide synthase - used  
 PT to prevent the hypotensive shock seen with sepsis.  
 PT  
 XX Disclosure: Fig 1; 53pp; English.  
 PS  
 XX AAQ66914 is from human hepatocyte inducible nitric oxide synthase cDNA  
 CC clone PHINOS from lambda Zap II cDNA library. The original source  
 CC was induced human hepatocyte RNA. HINOS cDNA plasmid is pref.  
 CC transformed in E. coli SOLR (ATCC 69126). The inventors claim a  
 CC clone with the cDNA sequence in AAQ66914 and a cDNA clone which  
 CC encodes AAR5764. The cloning and expression of a human tissue nitric  
 CC oxide synthase cDNA provides a source of the enzyme for therapeutic  
 CC purposes, for example to prevent the hypotensive shock seen with  
 CC sepsis.  
 XX  
 XX Sequence 1153 AA;  
 SQ  
  
 Query Match 94.8%; Score 92; DB 15; Length 1153;  
 Best Local Similarity 94.4%; Pred. No. 1e-06;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 RMTLVGSRPPDEH1YQ 18  
 ||||| ||||| |||||  
 Db 1009 rmtlvfgcrpdedhlyq 1026  
  
 RESULT 7  
 AAR63206  
 ID AAR63206 standard; Protein; 1153 AA.  
 XX  
 AC AAR63206;  
 XX  
 DT 09-MAY-1995 (first entry)  
 XX  
 XX Nitric-oxide-synthase.  
 DE  
 XX Nitric-oxide-synthase; NO-synthase; NOS; chondrocyte;  
 KW interleukin-1-beta; pBSHSINOS; arthritis; hypertension;  
 KW septic shock; inflammation; ischemia; dementia; obesity; tumor;  
 KW agonist; antagonist; vector; CHO; Chinese hamster ovary;  
 KW cell culture.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9423038-A.  
 PN  
 XX 13-OCT-1994.  
 PD  
 XX

PF 25-MAR-1994; 94WO-GB00621.  
 XX  
 PR 26-MAR-1993; 93GB-0006386.  
 XX  
 XX (WELL ) WELLCOME FOUND LTD.  
 PA  
 XX Charles IG, Moncada SE, Palmer RMJ, Moncada S;  
 PI  
 XX WPI: 1994-333198/41.  
 DR  
 XX N-PSDB; AAQ77700.  
 DR  
 XX New human inducible nitric oxide synthase - useful for  
 PT identifying enzyme inhibitors and stimulators, and for diagnosis  
 PT and treatment of e.g. viral infections or tumours  
 PT  
 XX Disclosure: Page 25-31; 42pp; English.  
 PS  
 XX Human chondrocytes were incubated with interleukin-1-beta to induce  
 CC nitric-oxide-synthase. cDNA was generated and used to construct a  
 CC library in lambda ZAPII. This was screened with a 650 bp fragment of  
 CC mouse inducible NO-synthase cDNA to identify the full-length clone  
 CC pBSHSINOS. The insert was transferred to pSVL to give a vector  
 CC capable of expressing NO-synthase in CHO cells under control of a  
 CC heterologous constitutive promoter.  
 XX  
 XX Sequence 1153 AA;  
 SQ  
  
 Query Match 94.8%; Score 92; DB 15; Length 1153;  
 Best Local Similarity 94.4%; Pred. No. 1e-06;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 RMTLVGSRPPDEH1YQ 18  
 ||||| ||||| |||||  
 Db 1009 rmtlvfgcrpdedhlyq 1026  
  
 RESULT 8  
 AAR88464  
 ID AAR88464 standard; Protein; 1153 AA.  
 XX  
 AC AAR88464;  
 XX  
 DT 13-MAY-1996 (first entry)  
 XX  
 XX Hepatocyte inducible nitric oxide synthase.  
 DE  
 XX Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy;  
 KW vascular occlusive disease; cancer; infection.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO9600006-A1.  
 PN  
 XX 04-JAN-1996.  
 PD  
 XX 20-JUN-1995; 95WO-US07849.  
 PF  
 XX 24-JUN-1994; 94US-0265046.  
 PR  
 XX (UYPI-) UNIV PITTSBURGH.  
 PA  
 XX Billiar TR, Geller DA, Nussler AK, Simmons RL, Tzeng E;  
 PI  
 XX WPI: 1996-068641/07.  
 DR  
 XX N-PSDB; AAT10115.  
 DR  
 XX Inducible nitric oxide synthase gene - useful in gene therapy to  
 PT treat, e.g. vascular occlusive disease and cancer  
 PT  
 XX Disclosure: Page 54-58; 91pp; English.  
 PS  
 XX An inducible nitric oxide synthase (iNOS = AAR88464) is the product  
 CC



CC of a cDNA clone (AA710115) derived from human hepatocytes induced  
 CC for iNOS biosynthesis. The iNOS can be obt'd. by expression of  
 CC the cDNA e.g. in mammalian host cells and is used in the  
 CC development of selective inhibitors of NOS or to treat diseases  
 CC affected by nitric oxide.

XX SQ Sequence 1153 AA;

Query Match 94.8%; Score 92; DB 17; Length 1153;  
 Best Local Similarity 94.4%; Pred. No. 1e-06;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RMTLVFGRSRPDEDHIYQ 18  
 ||||| ||||| |||||  
 Db 1009 rmtlvfgrcpdedhiyq 1026

RESULT 9  
 AAW36113  
 ID AAW36113 standard; Protein; 1153 AA.  
 AC AAW36113;  
 XX  
 DT 11-MAY-1998 (first entry)  
 DE Human inducible nitric oxide synthetase.  
 XX  
 KW Nitric oxide synthetase; NOS; iNOS; HPI NOS; human;  
 KW erectile dysfunction; impotence; gene therapy; corpora cavernosa;  
 KW relaxant.

XX OS Homo sapiens.  
 XX PN WO9742965-A1.  
 XX PD 20-NOV-1997.

XX PF 09-MAY-1997; 97WO-US07643.  
 XX PR 10-MAY-1996; 96US-0017373.  
 XX PA (GONZ/) GONZALEZ-CADAVID N F.  
 XX PA (RAJF/) RAJFER J.

XX PI Gonzalez-Cadavid NF, Rajfer J;  
 DR WPI: 1998-008577/01.  
 DR N-PSDB; AAT98199.

XX Treatment of erectile dysfunction - by introducing an agent into  
 PT penile tissue, particularly for inducing cavernosal smooth muscle  
 PT relaxation or increasing NOS levels

XX PS Claim 12; Page 38-41; 53pp; English.

XX This protein comprises human penis inducible nitric oxide  
 CC synthetase (HPI NOS). Its amino acid sequence was deduced from a  
 CC cDNA clone (see AAT98199) derived from human penile smooth muscle  
 CC cell mRNA. The invention is directed to a method of treating  
 CC erectile dysfunction in a patient by providing an agent capable of  
 CC treating erectile dysfunction, and introducing an effective amount  
 CC of the agent into the penile tissue of the patient. Preferably,  
 CC the agent induces cavernosal smooth muscle relaxation, and/or  
 CC produces an increase in the level of NOS in tissue. Preferably,  
 CC the NOS is iNOS, and the agent is introduced into the corpora  
 CC cavernosa of the penis. The agent is preferably an NOS inducer, an  
 CC NOS protein such as HPI NOS, a cDNA encoding an NOS such as HPI NOS,  
 CC or cDNA transformed penile cells, especially corpora cavernosa  
 CC cells.

XX SQ Sequence 1153 AA;

Query Match 94.8%; Score 92; DB 19; Length 1153;  
 Best Local Similarity 94.4%; Pred. No. 1e-06;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RMTLVFGRSRPDEDHIYQ 18  
 ||||| ||||| |||||  
 Db 1009 rmtlvfgrcpdedhiyq 1026

RESULT 10  
 AAB31724  
 ID AAB31724 standard; Protein; 1153 AA.

XX AC AAB31724;  
 XX DT 30-APR-2001 (first entry)

XX DE Amino acid sequence of a human inducible nitric oxide synthase (NOS).  
 KW Gene therapy; angiogenesis; nucleic acid delivery; arteriosclerosis;  
 KW nitric oxide synthase; NOS; endothelial dysfunction.

XX OS Homo sapiens.  
 XX PN WO200103728-A2.  
 XX PD 18-JAN-2001.

XX PF 07-JUL-2000; 2000WO-NL00482.  
 XX PR 09-JUL-1999; 99EP-0202263.  
 XX PR 09-JUL-1999; 99US-0143101.

XX PA (INTR-) INTROGENE BV.

XX PI Vogels R, Verlinden SFF;

XX DR WPI: 2001-123142/13.

XX Nucleic acid delivery vehicle comprising a nucleic acid encoding nitric  
 PT oxide synthase, used for isolated tissue perfusion treatment to enhance  
 PT and induce angiogenesis -

XX PS Disclosure; Fig 6; 37pp; English.

XX The specification describes a method for gene therapy for enhancing  
 CC and inducing angiogenesis. The method uses a nucleic acid delivery  
 CC vehicle, which comprises a nucleic acid encoding nitric oxide synthase  
 CC (NOS). The delivery vehicle is used for the manufacture of a  
 CC pharmaceutical composition for isolated tissue perfusion treatment.  
 CC The method is useful for enhancing and/or inducing angiogenesis in  
 CC patients with endothelial dysfunctions, in particular arteriosclerosis.  
 CC The present sequence represents an inducible NOS.

XX SQ Sequence 1153 AA;

Query Match 94.8%; Score 92; DB 22; Length 1153;  
 Best Local Similarity 94.4%; Pred. No. 1e-06;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RMTLVFGRSRPDEDHIYQ 18  
 ||||| ||||| |||||  
 Db 1009 rmtlvfgrcpdedhiyq 1026

RESULT 11  
 AAB66724  
 ID AAB66724 standard; protein; 1153 AA.

XX AC AAB66724;

```

DT 09-APR-2001 (first entry)
XX Human Inducible nitric oxide synthase.
DE
XX Nitric oxide synthase; NOS; angiogenesis; gene therapy.
KW
XX Homo sapiens.
OS
XX EP1067190-A1.
PN
XX 10-JAN-2001.
PD
XX 09-JUL-1999; 99EP-0202263.
PF
XX 09-JUL-1999; 99EP-0202263.
PR
XX (INTR-) INTROGENE BV.
PA
XX Vogels R, Verlinden S;
PI
XX WPI; 2001-125729/14.
DR
XX Use of a nucleic acid delivery vehicle comprising a nucleic acid
PT encoding nitric oxide synthase, especially useful in gene therapy for
PT enhancing and/or inducing angiogenesis and treating atherosclerosis -
PT
XX Examples; Page 14-18; 39pp; English.
PS
XX The present invention relates to use of a nucleic acid delivery
CC vehicle comprising a nucleic acid encoding nitric oxide synthase
CC (NOS) activity for the manufacture of a composition for essentially
CC isolated tissue perfusion treatment to enhance and/or induce
CC angiogenesis. The nucleic acid delivery vehicle is particularly
CC useful in gene therapy for the treatment of atherosclerosis.
XX
SQ Sequence 1153 AA;

Query Match 94.8%; Score 92; DB 22; Length 1153;
Best Local Similarity 94.4%; Pred. NO. 1e-06; Mismatches 0; Gaps 0;
Matches 17; Conservative 0; Indels 1;

QY 1 RMTLVGSRRPDEDH1YQ 18
| | | | | | | | | | | | | | | | | |
Db 1009 rmtlvfgcrpdedhiyq 1026

RESULT 12
AAW81255
ID AAW81255 standard; peptide; 15 AA.
XX
AC AAW81255;
XX
DT 30-APR-1999 (first entry)
XX
DE Human iNOS peptide fragment PS-5283.
XX
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 15
FT /note= "Gln residue amidated"
XX
XX W09845710-A1.
PN
XX 15-OCT-1998.
PD
XX
PF 11-APR-1997; 97WO-US06500.

```

```

XX 07-APR-1997; 97US-6667777.
PR (WEBB/) WEBBER R.
PA
XX Webber R;
PI
XX WPI; 1998-594495/50.
DR
XX Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
XX
PS Example 4; Page 39; 93pp; English.
XX
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention.
XX
SQ Sequence 15 AA;

Query Match 84.5%; Score 82; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. NO. 4.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVFGSRRPDEDH1YQ 18
| | | | | | | | | | | | | | | |
Db 1 lvfgsrpdedhiyq 15

RESULT 13
AAW81312
ID AAW81312 standard; peptide; 15 AA.
XX
AC AAW81312;
XX
DT 30-APR-1999 (first entry)
XX
DE Human iNOS peptide fragment for epitope mapping #33.
XX
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis; epitope mapping.
XX
OS Homo sapiens.
XX
PN W09845710-A1.
XX
PD 15-OCT-1998.
XX
PF 11-APR-1997; 97WO-US06500.
XX
PR 07-APR-1997; 97US-6667777.
XX
PA (WEBB/) WEBBER R.
XX
PI Webber R;
XX
XX WPI; 1998-594495/50.
DR
XX Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.

```

XX Example 4; Fig 7D; 93pp; English.

XX This invention describes an immunoassay method where a sample with a

CC specific binding entity (e.g. a monoclonal antibody) reactive to human

CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used

CC to detect the presence of human iNOS protein in the sample. The method

CC can be used for the detection and quantitation of human iNOS in cells and

CC tissues for various pathophysiological conditions such as sepsis, septic

CC shock, myocardial infarction, rejection of tissue in organs following

CC transplantation, monitoring "flare ups" in certain autoimmune diseases

CC such as lupus, psoriasis, and multiple sclerosis. This sequence

CC represents a peptide from human iNOS which is used in the method of the

CC invention.

XX SQ Sequence 15 AA;

Query Match 84.5%; Score 82; DB 19; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.1e-07; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVFGSRRPDEDHIYQ 18

DB 1 lvfgsrpdedhiyq 15

|||||

RESULT 14

AAW81259

ID AAW81259 standard; peptide; 15 AA.

XX AC AAW81259;

XX DT 30-APR-1999 (first entry)

XX DE Human iNOS peptide fragment PS-5287.

XX KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;

XX KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;

XX KW myocardial infarction; tissue rejection; transplantation; psoriasis;

XX KW autoimmune disease; multiple sclerosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 15

FT /note- "His residue amidated"

XX WO9845710-A1.

XX PD 15-OCT-1998.

XX PF 11-APR-1997; 97WO-US06500.

XX PR 07-APR-1997; 97US-6667777.

XX PA (WEBB/) WEBBER R.

XX PI Webber R;

XX WPI; 1998-594495/50.

XX PT Detection of human inducible nitric oxide synthase - using an

PT immunoassay in which a sample is contacted with a specific binding

PT entity reactive with human iNOS or mimics.

XX Example 4; Page 39; 93pp; English.

XX This invention describes an immunoassay method where a sample with a

CC specific binding entity (e.g. a monoclonal antibody) reactive to human

CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used

CC to detect the presence of human iNOS protein in the sample. The method

CC can be used for the detection and quantitation of human iNOS in cells and

CC tissues for various pathophysiological conditions such as sepsis, septic

CC shock, myocardial infarction, rejection of tissue in organs following

CC transplantation, monitoring "flare ups" in certain autoimmune diseases

CC such as lupus, psoriasis, and multiple sclerosis. This sequence

CC represents a peptide from human iNOS which is used in the method of the

CC invention.

XX SQ Sequence 15 AA;

Query Match 83.5%; Score 81; DB 19; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.9e-07; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMTLVFSGRRPDEDH 15

DB 1 rmtlvfsgrrpdedh 15

|||||

RESULT 15

AAW81316

ID AAW81316 standard; peptide; 15 AA.

XX AC AAW81316;

XX DT 30-APR-1999 (first entry)

XX DE Human iNOS peptide fragment for epitope mapping #37.

XX KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;

XX KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;

XX KW myocardial infarction; tissue rejection; transplantation; psoriasis;

XX KW autoimmune disease; multiple sclerosis; epitope mapping.

XX OS Homo sapiens.

XX PN WO9845710-A1.

XX PD 15-OCT-1998.

XX PF 11-APR-1997; 97WO-US06500.

XX PR 07-APR-1997; 97US-6667777.

XX PA (WEBB/) WEBBER R.

XX PI Webber R;

XX WPI; 1998-594495/50.

XX PT Detection of human inducible nitric oxide synthase - using an

PT immunoassay in which a sample is contacted with a specific binding

PT entity reactive with human iNOS or mimics.

XX Example 4; Fig 7D; 93pp; English.

XX This invention describes an immunoassay method where a sample with a

CC specific binding entity (e.g. a monoclonal antibody) reactive to human

CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used

CC to detect the presence of human iNOS protein in the sample. The method

CC can be used for the detection and quantitation of human iNOS in cells and

CC tissues for various pathophysiological conditions such as sepsis, septic

CC shock, myocardial infarction, rejection of tissue in organs following

CC transplantation, monitoring "flare ups" in certain autoimmune diseases

CC such as lupus, psoriasis, and multiple sclerosis. This sequence

CC represents a peptide from human iNOS which is used in the method of the

CC invention.

XX SQ Sequence 15 AA;

Query Match 83.5%; Score 81; DB 19; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.9e-07; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RMTLVGSRRPDEDH 15  
|||||  
Db 1 rmtlvfgrrrpdedh 15

Search completed: September 10, 2001, 14:00:25  
Job time: 169 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:11:14 ; Search time 72.54 Seconds  
(without alignments)  
32.830 Million cell updates/sec

Title: US-08-833-506C-32

Perfect score: 91

Sequence: 1 NNNVEKAPSATSSPVTQD 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP-archaea:\*
- 2: SP-bacteria:\*
- 3: SP-fungi:\*
- 4: SP-human:\*
- 5: SP-invertebrate:\*
- 6: SP-mammal:\*
- 7: SP-mhc:\*
- 8: SP-organelle:\*
- 9: SP-phage:\*
- 10: SP-plant:\*
- 11: SP-rodent:\*
- 12: SP-unclassified:\*
- 13: SP-vertebrate:\*
- 14: SP-virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	94.5	1114	4	O94994 homo sapien
2	71	78.0	1154	6	O97604 canis famil
3	68	74.7	1147	11	O9R0W4 Q9R0W4 rattus norv
4	68	74.7	1147	11	O9QW28 rattus sp.
5	54	59.3	1047	3	O93865 candida alb
6	47	51.6	758	3	O99299 saccharomyc
7	46	50.5	246	2	P72704 synechocyst
8	46	50.5	305	5	O9XWE0 Q9XWE0 caenorhabd
9	45	49.5	65	2	O9RHF6 Q9RHF6 acinetobact
10	45	49.5	65	2	O9R310 Q9R310 acinetobact
11	45	49.5	352	3	O74179 pleurotus o
12	45	49.5	652	10	O9Lk91 Q9Lk91 arabidopsis
13	44	48.4	504	4	O9Y5V9 Q9Y5V9 homo sapien
14	44	48.4	537	4	O9Y5W0 Q9Y5W0 homo sapien
15	44	48.4	563	4	O9Y5V8 Q9Y5V8 homo sapien
16	44	48.4	573	4	O9Y5V7 Q9Y5V7 homo sapien
17	44	48.4	596	4	O9Y250 Q9Y250 homo sapien
18	44	48.4	791	5	O00841 dictyosteli
19	44	48.4	796	3	O9Hfs7 kluyveromyc

20	44	48.4	905	3	O9P8C5	Q9P8C5 tolypocladi
21	43	47.3	349	1	O9VIB7	Q9VIB7 pyrococcus
22	43	47.3	539	4	O9NY99	Q9NY99 homo sapien
23	43	47.3	551	5	O9VLK8	Q9VLK8 drosophila
24	43	47.3	558	5	O9U1J8	Q9U1J8 drosophila
25	43	47.3	929	5	O9N993	Q9N993 leishmania
26	43	47.3	1045	3	O74473	O74473 schizosacch
27	42	46.2	115	5	O44040	O44040 plasmodium
28	42	46.2	115	5	O44047	O44047 plasmodium
29	42	46.2	132	3	O9HFD3	O9HFD3 phaffia rho
30	42	46.2	151	13	O9DFT8	O9DFT8 brachydanio
31	42	46.2	354	13	O9W6A8	O9W6A8 brachydanio
32	42	46.2	366	5	O18034	O18034 caenorhabdi
33	42	46.2	639	5	O9XV97	O9XV97 caenorhabdi
34	42	46.2	693	4	O9NYA7	O9NYA7 homo sapien
35	42	46.2	693	4	O9NYA3	O9NYA3 homo sapien
36	42	46.2	746	11	O88408	O88408 mus musculu
37	42	46.2	931	2	O9L655	O9L655 bacillus fi
38	42	46.2	1001	11	O9R0X5	O9R0X5 mus musculu
39	42	46.2	1096	3	O94174	O94174 pneumocysti
40	42	46.2	1247	5	O9VX80	O9VX80 drosophila
41	42	46.2	1251	13	O9DFT9	O9DFT9 brachydanio
42	42	46.2	2209	5	O97324	O97324 plasmodium
43	41.5	45.6	235	3	O9U004	O9U004 schizosacch
44	41	45.1	232	3	O93947	O93947 candida alb
45	41	45.1	236	4	O14761	O14761 homo sapien

ALIGNMENTS

RESULT 1

O94994 ID O94994 PRELIMINARY; PRT; 1114 AA.  
AC O94994: DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE INDUCIBLE NITRIC OXIDE SYNTHASE.  
GN INOS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ogawa Y., Nishijima S., Goto M., Ida M.;  
RT "Cloning and characterization of a novel splice variant of human  
inducible nitric oxide synthase."  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB022318; BAA37123.1;  
DR HSP; P35228; 4NOS.  
DR InterPro; IPR001094;  
DR InterPro; IPR001433;  
DR InterPro; IPR001709;  
DR InterPro; IPR003097;  
DR Pfam; PF00175; oxidored\_fad; 1.  
DR Pfam; PF00667; FAD\_binding; 1.  
DR PRINTS; PR00369; FLAVODOXIN.  
DR PRINTS; PR00371; FPNCR.  
SQ SEQUENCE 1114 AA; 126748 MW; C1F9624774435571 CRC64;

Query Match 94.5%; Score 86; DB 4; Length 1114;  
Best Local Similarity 94.4%; Pred. No. 7.4e-06;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18

Db 25 NNNVEKAPCATSSPVTQD 42

RESULT 2

```
O97604
ID O97604; PRELIMINARY; PRT; 1154 AA.
AC O97604;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE INDUCIBLE NITRIC OXIDE SYNTHASE.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=AORTA;
RX MEDLINE=98431941; PubMed=9746458;
RA Wang X., McGregor C.G.A., Miller V.M.;
RT "Induction and cDNA sequence of inducible nitric oxide synthase from
RT canine aortic smooth muscle cells.";
RL Am. J. Physiol. 275:H1122-H1129(1998).
DR EMBL; AF077821; AAC78630.1; -.
DR HSSP; P29477; INOS.
DR InterPro; IPR001094; -.
DR InterPro; IPR001433; -.
DR InterPro; IPR001709; -.
DR InterPro; IPR003097; -.
DR Pfam; PF00175; oxidored_fad; 1.
DR Pfam; PF00667; FAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
SQ SEQUENCE 1154 AA; 131709 MW; 42CD606E447254CB CRC64;

Query Match 78.0%; Score 71; DB 6; Length 1154;
Best Local Similarity 77.8%; Pred. No. 0.0023;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NNNVEKAPSATSSPVQTQD 18
Db 25 NNNVEKPGATPSPSTQD 42

RESULT 3
Q9ROW4
ID Q9ROW4; PRELIMINARY; PRT; 1147 AA.
AC Q9ROW4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE INDUCIBLE NITRIC OXIDE SYNTHASE.
GN INOS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR KYOTO;
RX MEDLINE=99326503; PubMed=10395902;
RA Keinänen R.A., Vartiainen N., Koistinen J.;
RT "Molecular cloning and characterization of the rat inducible nitric
RT oxide synthase (iNOS) gene.";
RL Gene 234:297-305(1999).
DR EMBL; AJ230462; CAB46089.1; -.
DR EMBL; AJ230463; CAB46089.1; JOINED.
DR EMBL; AJ230464; CAB46089.1; JOINED.
DR EMBL; AJ230465; CAB46089.1; JOINED.
DR EMBL; AJ230466; CAB46089.1; JOINED.
DR EMBL; AJ230467; CAB46089.1; JOINED.
DR EMBL; AJ230468; CAB46089.1; JOINED.
DR EMBL; AJ230469; CAB46089.1; JOINED.
DR EMBL; AJ230470; CAB46089.1; JOINED.
DR EMBL; AJ230471; CAB46089.1; JOINED.
DR EMBL; AJ230472; CAB46089.1; JOINED.
```

```
DR EMBL; AJ230473; CAB46089.1; JOINED.
DR EMBL; AJ230474; CAB46089.1; JOINED.
DR EMBL; AJ230475; CAB46089.1; JOINED.
DR EMBL; AJ230476; CAB46089.1; JOINED.
DR EMBL; AJ230477; CAB46089.1; JOINED.
DR EMBL; AJ230478; CAB46089.1; JOINED.
DR EMBL; AJ230479; CAB46089.1; JOINED.
DR EMBL; AJ230480; CAB46089.1; JOINED.
DR EMBL; AJ230481; CAB46089.1; JOINED.
DR EMBL; AJ230482; CAB46089.1; JOINED.
DR EMBL; AJ230483; CAB46089.1; JOINED.
DR EMBL; AJ230484; CAB46089.1; JOINED.
DR EMBL; AJ230485; CAB46089.1; JOINED.
DR EMBL; AJ230486; CAB46089.1; JOINED.
DR HSSP; P29477; INOS.
DR InterPro; IPR001094; -.
DR InterPro; IPR001433; -.
DR InterPro; IPR001709; -.
DR InterPro; IPR003097; -.
DR Pfam; PF00175; oxidored_fad; 1.
DR Pfam; PF00667; FAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
SQ SEQUENCE 1147 AA; 130613 MW; E76B3F8407D54CF6 CRC64;

Query Match 74.7%; Score 68; DB 11; Length 1147;
Best Local Similarity 72.2%; Pred. No. 0.0071;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 NNNVEKAPSATSSPVQTQD 18
Db 25 NNNVEKPGATPSPSTQD 42

RESULT 4
Q9QW28
ID Q9QW28; PRELIMINARY; PRT; 1147 AA.
AC Q9QW28;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE CYTOKINE INDUCIBLE NITRIC OXIDE SYNTHASE, INOS.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93221515; PubMed=7682072;
RA Wood E.R., Berger H.Jr., Sherman P.A., Lapetina E.G.;
RT "Hepatocytes and macrophages express an identical cytokine inducible
RT nitric oxide synthase gene.";
RL Biochem. Biophys. Res. Commun. 191:767-774(1993).
DR HSSP; P29477; INOS.
DR InterPro; IPR001094; -.
DR InterPro; IPR001433; -.
DR InterPro; IPR001709; -.
DR InterPro; IPR002369; -.
DR InterPro; IPR003097; -.
DR Pfam; PF00175; oxidored_fad; 1.
DR Pfam; PF00667; FAD_binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PRODOM; PD001811; -. 1.
SQ SEQUENCE 1147 AA; 130625 MW; 2CAF8983E56F651A CRC64;

Query Match 74.7%; Score 68; DB 11; Length 1147;
Best Local Similarity 72.2%; Pred. No. 0.0071;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

QY 1 NNNVEKAPSTSSPVTD 18  
 ||||| | | | | |  
 Db 25 NNNVETPGAIPSTTD 42

RESULT 5  
 O93865 PRELIMINARY; PRT; 1047 AA.  
 AC O93865;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
 DE AGGLUTININ-LIKE CELL SURFACE PROTEIN.  
 GN ALS7.  
 OS Candida albicans (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCBI\_TaxID=5476;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC10261;  
 RA Leng P., Brown A.J.P.;  
 RT "The hyphal-specific gene ALS7 is a member of a Candida albicans gene  
 family encoding agglutinin-like cell surface proteins";  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF051313; AAD02580.1; -  
 SQ SEQUENCE 1047 AA; 111944 MW; C2327659AA911F2E CRC64;

Query Match 59.3%; Score 54; DB 3; Length 1047;  
 Best Local Similarity 75.0%; Pred. No. 1.3;  
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 NNNVEKAPSTSSPVT 16  
 || ||||| | | | | |  
 Db 957 NNGGKAPSTSSPST 972

RESULT 6  
 Q99299 PRELIMINARY; PRT; 758 AA.  
 AC Q99299;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE P2570 PROTEIN.  
 GN YPL158C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB972;  
 RA Purnelle B., Combiez S., Coster F., Naveau F., Goffeau A.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MIPS;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: X96770; CAA65563.1; -  
 DR EMBL: Z73514; CAA97863.1; -  
 DR SGD: S0006079; YPL158C.  
 SQ SEQUENCE 758 AA; 84845 MW; 3B4FA92B91C87F2B CRC64;

Query Match 51.6%; Score 47; DB 3; Length 758;  
 Best Local Similarity 60.0%; Pred. No. 14;  
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 NVEKAPSTSSPVTD 17  
 ||||| | | | | |  
 Db 309 NVOKVFSATNSKTK 323

RESULT 7  
 P72704 PRELIMINARY; PRT; 246 AA.  
 AC P72704;  
 DT 01-JAN-1999 (TrEMBLrel. 09, Created)  
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B (EC 5.2.1.8) (PPIASE B)  
 DE (ROTAMASE B).  
 GN PPIB.  
 OS Synechocystis sp. (Strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OX NCBI\_TaxID=1143;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,  
 RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 entire genome and assignment of potential protein-coding regions";  
 RL DNA Res. 3:109-136(1996).  
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.  
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
 PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -!- ENZYME REGULATION: INHIBITED BY CYCLOSPORIN A (CSA).  
 CC -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.  
 DR EMBL: D90900; BAA16711.1; -  
 DR HSSP: P20752; ICLH.  
 DR InterPro: IPR002130; -  
 DR Pfam: PF00160; pro\_isomerase\_2.  
 DR PROSITE: PS00170; CSA\_PPIASE\_1; 1.  
 DR PROSITE: PS50072; CSA\_PPIASE\_2; 1.  
 DR KW Hypothetical protein; Isomerase; Rotamase.  
 SQ SEQUENCE 246 AA; 26580 MW; 02080EE3C339932F CRC64;

Query Match 50.5%; Score 46; DB 2; Length 246;  
 Best Local Similarity 47.1%; Pred. No. 6.9;  
 Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NNNVEKAPSTSSPVTD 17  
 || | | | | | | | | |  
 Db 33 NSSAEFSPTETNSPVAQ 49

RESULT 8  
 Q9XWE0 PRELIMINARY; PRT; 305 AA.  
 ID Q9XWE0  
 AC Q9XWE0;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Y47H9C.6 PROTEIN.  
 GN Y47H9C.6.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Harris B.R.;  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C.elegans: A platform for

RT investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL; AL032657; CAA21735.2; -.  
 DR HSSP; P42574; 1CP3  
 DR InterPro; IPR002138; -.  
 DR Pfam; PF00655; ICE\_P10; 1.  
 SQ SEQUENCE 305 AA; 35084 MW; 6D8A0D840B832416 CRC64;

Query Match 50.5%; Score 46; DB 5; Length 305;  
 Best Local Similarity 57.1%; Pred. No. 8.5;  
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 EKAPSATSSPVTD 18

DB 170 DPGPTASSSPLTQD 183

RESULT 9

Q9RHF6 PRELIMINARY; PRT; 65 AA.  
 AC Q9RHF6;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE URF-1 PROTEIN (FRAGMENT).  
 GN URF-1.  
 OS Acinetobacter calcoaceticus.  
 OG Plasmid pKLH1.  
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;  
 OC Acinetobacter.  
 OX NCBI\_TaxID=471;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TRANSPOSON-ABERRANT MERCURY RESISTANCE TRANSPOSON;  
 RA Kholodii G.Y., Mindlin S.Z., Lomovskaya O.L., Gorlenko Z.M.,  
 RA Yurieva O.V., Nikiforov V.G.;  
 RT "pKLH1-like aberrant mercury resistance transposons of environmental  
 RT Acinetobacter strains: spread, polymorphism and possible origin."  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ251518; CAB65944.1; -.  
 KW Plasmid.  
 FT NON\_TER  
 SQ SEQUENCE 65 AA; 6837 MW; BF777CE1A70C4DB5 CRC64;

Query Match 49.5%; Score 45; DB 2; Length 65;

Best Local Similarity 53.3%; Pred. No. 2.8;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 NNVEKAPSATSSPVT 16

DB 2 NNPERLPSETHKPIT 16

RESULT 10

Q9R310 PRELIMINARY; PRT; 65 AA.  
 AC Q9R310;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE URF-1 PROTEIN (FRAGMENT).  
 GN URF-1.  
 OS Acinetobacter lwoffii.  
 OG Plasmid pKLH103, plasmid pKLH102, and Plasmid pKLH104.  
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;  
 OC Acinetobacter.  
 OX NCBI\_TaxID=28090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kholodii G.Y., Mindlin S.Z., Lomovskaya O.L., Gorlenko Z.M.,  
 RA Yurieva O.V., Nikiforov V.G.;

RT "pKLH1-like aberrant mercury resistance transposons of environmental  
 RT Acinetobacter strains: spread, polymorphism and possible origin."  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ251540; CAB65956.1; -.  
 DR EMBL; AJ250011; CAB65948.1; -.  
 DR EMBL; AJ251538; CAB65952.1; -.  
 DR InterPro; IPR002218; -.  
 DR ProDom; PD003738; -; 1.  
 KW Plasmid.  
 FT NON\_TER  
 SQ SEQUENCE 65 AA; 6837 MW; BF777CE1A70C4DB5 CRC64;

Query Match 49.5%; Score 45; DB 2; Length 65;

Best Local Similarity 53.3%; Pred. No. 2.8;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 NNVEKAPSATSSPVT 16

DB 2 NNPERLPSETHKPIT 16

RESULT 11

O74179 PRELIMINARY; PRT; 352 AA.  
 AC O74179;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAY-2001 (TREMBLrel. 16, Last annotation update)  
 DE MANGANESE PEROXIDASE (MNP3).  
 GN MNP3.  
 OS Pleurotus ostreatus (Oyster mushroom) (White-rot fungus).  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Agaricales;  
 OC Pleurotaceae; Pleurotus.  
 OX NCBI\_TaxID=5322;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Irie T., Honda Y., Matsuyama T., Watanabe T., Kuwahara M.;  
 RT "Genomic sequence encoding manganese peroxidase isozyme, Mnp3 from the  
 RT white-rot basidiomycete, Pleurotus ostreatus."  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB016519; BAA33009.2; -.  
 DR HSSP; P06181; 1B85.  
 DR InterPro; IPR002016; -.  
 DR Pfam; PF00141; peroxidase; 1.  
 DR PRINTS; PR00458; PEROXIDASE.  
 DR PROSITE; PS00435; PEROXIDASE\_1; 1.  
 DR PROSITE; PS00436; PEROXIDASE\_2; UNKNOWN\_1.  
 KW Peroxidase.  
 SQ SEQUENCE 352 AA; 36908 MW; E521F96E3B96E131 CRC64;

Query Match 49.5%; Score 45; DB 3; Length 352;

Best Local Similarity 53.8%; Pred. No. 14;

Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 NNVEKAPSATSSP 14

DB 328 NNIEQAPALTADP 340

RESULT 12

O9LK91 PRELIMINARY; PRT; 652 AA.  
 AC O9LK91;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE GB|AAF23297.1  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.



```
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Structure features of the regions of 4,251,695 bp covered by ninety pl,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP000371; BAB02532.1; -.
DR InterPro; IPR000313; -.
DR InterPro; IPR001848; -.
DR ProDom; PD001272; -.
SQ SEQUENCE 652 AA; 73666 MW; D567964FFEF1F4CE6 CRC64;

Query Match 49.5%; Score 45; DB 10; Length 652;
Best Local Similarity 56.2%; Pred. No. 26;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSPVTQD 16
Db 567 NRSLEKCPFATTSTVT 582

RESULT 13
ID Q9Y5V9 PRELIMINARY; PRT; 504 AA.
AC Q9Y5V9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE FEZ1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99199287; PubMed=10097140;
RA Ishii H., Baffa R., Numata S.I., Murakumo Y., Rattan S., Inoue H.,
RA Mori M., Fidanza V., Alder H., Croce C.M.;
RT "The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
RT and its expression is altered in multiple human tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:3928-3933(1999).
DR EMBL; AF123656; AAD23837.1; -.
SQ SEQUENCE 504 AA; 55611 MW; 6665CACB72272BC0 CRC64;

Query Match 48.4%; Score 44; DB 4; Length 504;
Best Local Similarity 38.9%; Pred. No. 29;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSPVTQD 18
Db 242 SNKADKGPSCVRSPISTD 259

RESULT 14
ID Q9Y5W0 PRELIMINARY; PRT; 537 AA.
AC Q9Y5W0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE FEZ1.
```

```
GN FEZ1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99199287; PubMed=10097140;
RA Ishii H., Baffa R., Numata S.I., Murakumo Y., Rattan S., Inoue H.,
RA Mori M., Fidanza V., Alder H., Croce C.M.;
RT "The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
RT and its expression is altered in multiple human tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:3928-3933(1999).
DR EMBL; AF123655; AAD23836.1; -.
SQ SEQUENCE 537 AA; 59829 MW; CE0F771B1629051B CRC64;
```

Query Match 48.4%; Score 44; DB 4; Length 537;  
Best Local Similarity 38.9%; Pred. No. 31;  
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSPVTQD 18  
Db 242 SNKADKGPSCVRSPISTD 259

```
RESULT 15
ID Q9Y5V8 PRELIMINARY; PRT; 563 AA.
AC Q9Y5V8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE FEZ1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99199287; PubMed=10097140;
RA Ishii H., Baffa R., Numata S.I., Murakumo Y., Rattan S., Inoue H.,
RA Mori M., Fidanza V., Alder H., Croce C.M.;
RT "The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
RT and its expression is altered in multiple human tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:3928-3933(1999).
DR EMBL; AF123657; AAD23838.1; -.
SQ SEQUENCE 563 AA; 62910 MW; E6EF5D260E41380C CRC64;
```

Query Match 48.4%; Score 44; DB 4; Length 563;  
Best Local Similarity 38.9%; Pred. No. 33;  
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSPVTQD 18  
Db 242 SNKADKGPSCVRSPISTD 259

Search completed: September 10, 2001, 14:11:15  
Job time: 594 sec

**This Page Blank (usp10)**

GenCore version 4.5  
Copyright (c) 1993 - 2000, CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:09:54 ; Search time 23.82 Seconds  
(without alignments)  
25.886 Million cell updates/sec

Title: US-08-833-506C-32

Perfect score: 91

Sequence: 1 NNNVERAPSATSSPVTQD 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	94.5	1153	1 NS2A_HUMAN	P35228 homo sapien
2	68	74.7	1147	1 NOS2_RAT	O06518 rattus norv
3	68	74.7	1147	1 NS2D_HUMAN	O60591 homo sapien
4	65	71.4	162	1 NOS2_MACMU	O48660 macaca mula
5	57	62.6	1144	1 NOS2_MOUSE	P29477 mus musculus
6	54	59.3	1119	1 ALS3_CANAL	O74623 candida alb
7	45	49.5	78	1 MERE_PSEAE	P06690 pseudomonas
8	44	48.4	982	1 HBL1_CAEEL	O9xyd3 caenorhabdi
9	44	48.4	1338	1 CEK1_SCHPO	P38938 schizosacch
10	44	48.4	3149	1 TEGU_EBV	P03186 epstein-bar
11	43.5	47.8	677	1 VGP_EBORE	O66799 ebola virus
12	43.5	47.8	677	1 VGP_EBORS	O89853 ebola virus
13	43.5	47.8	3329	1 BRG2_MOUSE	P97929 mus musculus
14	42	46.2	438	1 LNK3_CAEEL	O03345 caenorhabdi
15	41.5	45.6	428	1 YS45_CAEEL	O09660 caenorhabdi
16	41.5	45.6	767	1 CC10_SCHPO	P01129 schizosacch
17	41	45.1	581	1 PME3_PSHAV	O43111 phaseolus v
18	40.5	44.5	965	1 AKPN3_RABIT	P15541 oryctolagus
19	40.5	44.5	993	1 TSH_DROME	P22265 drosophila
20	40	44.0	351	1 OPSB_CARAU	P32310 carassius a
21	40	44.0	427	1 DAMX_ECOLI	P11557 escherichia
22	40	44.0	591	1 GV7_XENLA	P20398 xenopus lae
23	40	44.0	727	1 BRCL_DROME	O01295 drosophila
24	39	42.9	140	1 BM88_PIG	Q29026 sus scrofa
25	39	42.9	238	1 F801_SCHMA	P16463 schistosoma
26	39	42.9	248	1 IFE3_CAEEL	O61955 caenorhabdi
27	39	42.9	342	1 YW22_YEAST	P40214 saccharomyc
28	39	42.9	436	1 YIN5_YEAST	P40463 saccharomyc
29	39	42.9	444	1 YFHA_ECOLI	P21712 escherichia
30	39	42.9	475	1 YFHA_YEAST	Q00776 saccharomyc
31	39	42.9	563	1 GUNB_CLOTM	P04956 clostridium
32	39	42.9	743	1 TLE2_HUMAN	O04725 homo sapien
33	39	42.9	1140	1 YW96_YEAST	Q04893 saccharomyc

34	39	42.9	1905	1 TAGB_DICDI	P54683 dictyosteli
35	38	41.8	94	1 YOF3_CAEEL	P34661 caenorhabdi
36	38	41.8	98	1 TATA_RHOER	P72267 rhodococcus
37	38	41.8	251	1 Y095_HAEIN	Q57060 haemophilus
38	38	41.8	253	1 UPPS_CHLFR	O84456 chlamydia t
39	38	41.8	287	1 SCF_CHICK	Q09108 gallus gall
40	38	41.8	291	1 SPI3_YEAST	P23624 saccharomyc
41	38	41.8	449	1 GAT6_HUMAN	Q92908 homo sapien
42	38	41.8	579	1 YKM4_YEAST	P32343 saccharomyc
43	38	41.8	687	1 FSHR_EQUAS	Q95179 equus asinu
44	38	41.8	692	1 FSHR_RAT	P20395 rattus norv
45	38	41.8	694	1 FSHR_HORSE	P47799 equus cabal

#### ALIGNMENTS

RESULT 1  
NS2A\_HUMAN  
ID NS2A\_HUMAN STANDARD; PRT; 1153 AA.  
AC P35228; Q16692; O60757; Q16263;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)  
DE (INDUCIBLE NOS) (INOS) (HEPATOCYTE NOS) (HEP-NOS).  
GN NOS2A OR NOS2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=932334523; PubMed=7682706;  
RA Geller D.A., Lowenstein C.J., Shapiro R.A., Nussler A.K.,  
RA di Silvio M., Wang S.C., Nakayama D.K., Simmons R.L., Snyder S.H.,  
RA Billiar T.R.;  
RT "Molecular cloning and expression of inducible nitric oxide synthase  
from human hepatocytes.";  
RT Proc. Natl. Acad. Sci. U.S.A. 90:3491-3495(1993).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Colorectal adenocarcinoma;  
RX MEDLINE=94032282; PubMed=7692964;  
RA Sherman P.A., Laubach V.E., Reep B.R., Wood E.R.;  
RT "Purification and cDNA sequence of an inducible nitric oxide synthase  
from a human tumor cell line.";  
RL Biochemistry 32:11600-11605(1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Chondrocytes;  
RX MEDLINE=94068614; PubMed=7504305;  
RA Charles I.G., Palmer R.M.J., Hickery M.S., Bayliss M.T.,  
RA Chubb A.P., Hall V.S., Moss D.W., Moncada S.;  
RT "Cloning, characterization, and expression of a cDNA encoding an  
inducible nitric oxide synthase from the human chondrocyte.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:11419-11423(1993).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Articular chondrocytes;  
RX MEDLINE=94368816; PubMed=7522054;  
RA Maier R., Bilbe G., Rediske J., Lotz M.;  
RT "Inducible nitric oxide synthase from human articular chondrocytes:  
cDNA cloning and analysis of mRNA expression.";  
RL Biochim. Biophys. Acta 1208:145-150(1994).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Retina;  
RX MEDLINE=95091827; PubMed=7528017;  
RA Park C.S., Pardhasaradhi K., Gianotti C., Villegas E., Krishna G.;  
RT "Human retina expresses both constitutive and inducible isoforms of  
nitric oxide synthase mRNA.";

Biochem. Biophys. Res. Commun. 205:85-91(1994).  
 [6]  
 RN SEQUENCE FROM N.A.  
 RP  
 RC TISSUE-Glioblastoma;  
 RX MEDLINE=95155267; PubMed=7531687;  
 RA Hokari A., Zeniya M., Esumi H.;  
 RT "Cloning and functional expression of human inducible nitric oxide  
 RT synthase (NOS) cDNA from a glioblastoma cell line A-172.";  
 RL J. Biochem. 116:575-581(1994).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE-Airway epithelium;  
 RX MEDLINE=95372368; PubMed=7544004;  
 RA Guo F.H., de Raeye R.H., Rice T.W., Stuehr D.J., Thunnissen F.B.J.M.,  
 RA Erzurum S.C.;  
 RT "Continuous nitric oxide synthesis by inducible nitric oxide synthase  
 RT in normal human airway epithelium in vivo.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7809-7813(1995).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE-Cardiac myocytes;  
 RX MEDLINE=97304504; PubMed=9160867;  
 RA Luss H., Li R.-K., Shapiro R.A., Tzeng E., McGowan F.X., Yoneyama T.,  
 RA Hatakayama K., Geller D.A., Mickie D.A.G., Simmons R.L.,  
 RA Billiar T.R.;  
 RT "Dedifferentiated human ventricular cardiac myocytes express  
 RT inducible nitric oxide synthase mRNA but not protein in response to  
 RT IL-1, TNF, IFN-gamma, and LPS.";  
 RL J. Mol. Cell. Cardiol. 29:1153-1165(1997).  
 RN [9]  
 RP SEQUENCE OF 380-473 FROM N.A.  
 RP TISSUE-Kidney;  
 RX MEDLINE=95165725; PubMed=7532248;  
 RA McLeay J.S., Chatterjee P., Nicolson A.G., Jardine A.G., McKay N.G.,  
 RA Ralston S.H., Grabow P., Hailstones N.E., Macleod A.M.,  
 RA Hawksworth G.M.;  
 RT "Nitric oxide production by human proximal tubular cells: a novel  
 RT immunomodulatory mechanism?";  
 RL Kidney Int. 46:1043-1049(1994).  
 RN [10]  
 RP CHARACTERIZATION.  
 RX MEDLINE=96047340; PubMed=7558036;  
 RA Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G.,  
 RA Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;  
 RT "Three members of the nitric oxide synthase II gene family (NOS2A,  
 RT NOS2B, and NOS2C) colocalize to human chromosome 17.";  
 RL Genomics 27:526-530(1995).  
 RN [11]  
 RP CHARACTERIZATION.  
 RX MEDLINE=98398865; PubMed=9721329;  
 RA Taylor B.S., Alarcon L.H., Billiar T.R.;  
 RT "Inducible nitric oxide synthase in the liver: regulation and  
 RT function.";  
 RL Biochimica 63:766-781(1998).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 74-504.  
 RX MEDLINE=99340067; PubMed=10409685;  
 RA Li H., Raman C.S., Glaser C.B., Blasko E., Young T.A., Parkinson J.F.,  
 RA Whitlow M., Poulos T.L.;  
 RT "Crystal structures of zinc-free and -bound heme domain of human  
 RT inducible nitric-oxide synthase. Implications for dimer stability and  
 RT comparison with endothelial nitric-oxide synthase.";  
 RL J. Biol. Chem. 274:21276-21284(1999).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 82-528.  
 RX MEDLINE=99173237; PubMed=10074942;  
 RA Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,  
 RA Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,  
 RA Weber P.C.;  
 RT "Structural characterization of nitric oxide synthase isoforms  
 RT reveals striking active-site conservation.";  
 RL Nat. Struct. Biol. 6:233-242(1999).  
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE

WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO  
 MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.  
 -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + H<sup>+</sup> O(2) - CITRULLINE +  
 NITRIC OXIDE + N NADP(+).  
 -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 THE ENZYME (BY SIMILARITY).  
 -1- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST  
 WITH MOUSE NOS2). ASPIRIN INHIBITS EXPRESSION AND FUNCTION OF THIS  
 ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF  
 TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE  
 CATALYTIC ACTIVITY (BY SIMILARITY).  
 -1- SUBUNIT: HOMODIMER.  
 -1- TISSUE SPECIFICITY: EXPRESSED IN THE LIVER, RETINA, BONE CELLS AND  
 AIRWAY EPITHELIAL CELLS OF THE LUNG. NOT EXPRESSED IN THE  
 PLATELETS.  
 -1- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES.  
 -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 -----  
 This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 EMBL; L09210; AAA59171.1; -;  
 EMBL; L24553; AAA36375.1; -;  
 EMBL; X73029; CAA51512.1; -;  
 EMBL; U05810; AAA56666.1; -;  
 EMBL; U31511; AAB49041.1; -;  
 EMBL; D26525; BAA05531.1; -;  
 EMBL; U20441; AAB60366.1; -;  
 EMBL; AF068236; AAC19133.1; -;  
 EMBL; S75615; AAD14179.1; -;  
 PIR; A47475; A47475.  
 PDB; 1NSI; 07-JAN-00.  
 PDB; 2NSI; 07-JAN-00.  
 PDB; 4NOS; 04-FEB-00.  
 MIM; 163730; -;  
 DR InterPro; IPR001094; -;  
 DR InterPro; IPR001433; -;  
 DR InterPro; IPR001709; -;  
 DR InterPro; IPR003097; -;  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR Pfam; PF00175; oxidored\_fad; 1.  
 DR PRINTS; PR00369; FLAVOPODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 KW Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;  
 KW Heme; Phosphorylation; Zinc; Metal-binding; Multigene family;  
 KW 3D-structure.  
 FT BINDING 200  
 FT DOMAIN 509  
 FT NP\_BIND 623  
 FT NP\_BIND 767  
 FT NP\_BIND 903  
 FT NP\_BIND 978  
 FT NP\_BIND 1076  
 FT METAL 110  
 FT METAL 115  
 FT MOD\_RES 234  
 FT MOD\_RES 578  
 FT MOD\_RES 892  
 FT CONFLICT 23  
 FT CONFLICT 154  
 FT CONFLICT 177  
 FT CONFLICT 266  
 FT CONFLICT 423  
 FT CONFLICT 439  
 FT CONFLICT 608  
 FT CONFLICT 676  
 FT CONFLICT 800  
 HEME.  
 CALMODULIN-BINDING (POTENTIAL).  
 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FAD (ADP PART) (BY SIMILARITY).  
 FAD (FLAVIN PART) (BY SIMILARITY).  
 NADP (RIBOSE PART) (BY SIMILARITY).  
 NADP (ADP PART) (BY SIMILARITY).  
 ZINC.  
 ZINC.  
 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 D -> G (IN REF. 4).  
 F -> L (IN REF. 4).  
 G -> V (IN REF. 4).  
 R -> H (IN REF. 8).  
 L -> I (IN REF. 2).  
 A -> T (IN REF. 8).  
 S -> L (IN REF. 5 AND 6).  
 T -> I (IN REF. 7).  
 T -> A (IN REF. 4).

Query Match 94.5%; Score 86; DB 1; Length 1153;  
 Best Local Similarity 94.4%; Pred. No. 6.5e-06;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTD 18  
 Db 25 NNNVEKAPCATSSPVTD 42

RESULT 2  
 NOS2\_RAT  
 ID NOS2\_RAT STANDARD; PRT: 1147 AA  
 AC Q06518; P97774; Q35765; Q35766; Q64558; Q64005; Q63267;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE NITRIC OXIDE SYNTHASE, INDUCIBLE (BC 1.14.13.39) (NOS, TYPE II)  
 DE (INDUCIBLE NOS) (INOS).  
 GN NOS2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Vascular smooth muscle;  
 RX MEDLINE=93191721; PubMed=7680561;  
 RA Nunokawa Y., Ishida N., Tanaka S.;  
 RT "Cloning of inducible nitric oxide synthase in rat vascular smooth  
 muscle cells";  
 RL Biochem. Biophys. Res. Commun. 191:89-94(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar; TISSUE=Pancratic islets;  
 RX MEDLINE=95309542; PubMed=7540573;  
 RA Karlisen A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J.,  
 RA Cuatrecasas B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,  
 RA Mandrup-Poulsen T., Boel E., Nerup J.;  
 RT "Cloning and expression of cytokine-inducible nitric oxide synthase  
 cDNA from rat islets of Langerhans";  
 RL Diabetes 44:753-758(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Astrocytes;  
 RX MEDLINE=94231594; PubMed=7513765;  
 RA Galea E., Reis D.J., Feinstein D.L.;  
 RT "Cloning and expression of inducible nitric oxide synthase from rat  
 astrocytes";  
 RL J. Neurosci. Res. 37:406-414(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=94039059; PubMed=7693462;  
 RA Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K.,  
 RA Kawasaki H., Sugimura T., Esumi H.;  
 RT "Molecular cloning of a cDNA encoding an inducible  
 calmodulin-dependent nitric-oxide synthase from rat liver and its  
 expression in COS 1 cells";  
 RL Eur. J. Biochem. 217:37-43(1993).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Hepatocytes;  
 RX MEDLINE=93221515; PubMed=7682072;  
 RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;  
 RT "Hepatocytes and macrophages express an identical cytokine inducible  
 nitric oxide synthase gene";  
 RL Biochem. Biophys. Res. Commun. 191:767-774(1993).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Aorta;  
 RX MEDLINE=94325351; PubMed=7519448;  
 RA Geng Y.J., Almqvist M., Hansson G.K.;

RT "cDNA cloning and expression of inducible nitric oxide synthase from  
 rat vascular smooth muscle cells";  
 RL Biochim. Biophys. Acta 1218:421-424(1994).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Kosuga K., Yui Y., Hattori R., Sase K., Eizawa H., Aoyama T.,  
 RA Inoue R., Sasayama S.;  
 RT "Cloning of an inducible nitric oxide synthase from rat  
 polymorphonuclear neutrophils";  
 RL Endothelium 2:217-221(1994).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97070590; PubMed=8913516;  
 RA Tsusumishita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,  
 RA Futaki S., Niwa M.;  
 RT "Sequence analysis of inducible nitric oxide synthase in rat kidney,  
 lung, and uterus";  
 RL Biol. Pharm. Bull. 19:1374-1376(1996).  
 RN [9]  
 RP SEQUENCE OF 426-788 FROM N.A.  
 RC STRAIN=DAHL/RAPP SALT SENSITIVE STRAIN; TISSUE=Vascular smooth muscle;  
 RX MEDLINE=98195092; PubMed=9535415;  
 RA Chen P.Y., Gladish R.D., Sanders P.W.;  
 RT "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp  
 salt-sensitive rats";  
 RL Hypertension 31:918-924(1998).  
 RN [10]  
 RP SEQUENCE OF 509-740 FROM N.A.  
 RC STRAIN=Wistar; TISSUE=Renal glomerulus;  
 RA Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;  
 RT "Advances in the studies of NO synthesis regulation in mesangial  
 cells";  
 RL Nephrologia 16:35-39(1996).  
 RN [11]  
 RP SEQUENCE OF 479-655 FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Renal glomerulus;  
 RX MEDLINE=94276509; PubMed=7516453;  
 RA Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montani D.,  
 RA Klahr S.;  
 RT "Location of an inducible nitric oxide synthase mRNA in the normal  
 kidney";  
 RL Kidney Int. 45:998-1005(1994).  
 RN [12]  
 RP SEQUENCE OF 420-479 FROM N.A.  
 RC TISSUE=Myocardium;  
 RA Michel T., Balligand J.-L.;  
 RT "Isolation and characterization of iNOS from rat cardiocytes";  
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
 WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.  
 CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +  
 NITRIC OXIDE + N NADP(+).  
 CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
 TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
 THE ENZYME.  
 CC -!- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPRIN  
 INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE  
 EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL  
 MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY  
 SIMILARITY).  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- TISSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY IN THE  
 MEDULLARY THICK ASCENDING LOOP, WITH MINOR AMOUNTS IN THE  
 MEDULLARY COLLECTING DUCT AND VASA RECTA BUNDLE.  
 CC -!- INDUCTION: BY INTERFERON GAMMA AND LIPOPOLYSACCHARIDE.  
 CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

```

CC  EMBL; D14051; BAA03138.1; -
CC  EMBL; U26886; AAR85861.1; -
DR  EMBL; U03699; AAC13747.1; -
DR  EMBL; D12520; BAA02090.1; -
DR  EMBL; L12562; AAA41720.1; -
DR  EMBL; X76881; CAA54208.1; -
DR  EMBL; D44591; BAA07994.1; -
DR  EMBL; D83661; BAA12035.1; -
DR  EMBL; AF006619; AAC16401.1; -
DR  EMBL; AF006620; AAC16402.1; -
DR  EMBL; U48829; AAB18620.1; -
DR  EMBL; S71597; AAB31028.2; -
DR  EMBL; L36063; AAC02242.1; -
DR  PIR; JCI472; JCI472; -
DR  HSP; P29477; INOC.
DR  InterPro; IPR001094; -
DR  InterPro; IPR001433; -
DR  InterPro; IPR001709; -
DR  InterPro; IPR003097; -
DR  Pfam; PF00667; FAD_binding; 1.
DR  Pfam; PF00175; oxidored_fad; 1.
DR  PRINTS; PR00369; FLAVODOXIN.
DR  PRINTS; PR00371; FPNCR.
KW  Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
KW  Zinc; Metal-binding; Multigene family.
FT  BINDING 197 197
FT  DOMAIN 506 526
FT  NP_BIND 620 651
FT  NP_BIND 764 775
FT  NP_BIND 900 910
FT  NP_BIND 975 993
FT  NP_BIND 1073 1088
FT  METAL 107 107
FT  METAL 112 112
FT  CONFLICT 10 10
FT  CONFLICT 72 72
FT  CONFLICT 107 107
FT  CONFLICT 128 128
FT  CONFLICT 130 130
FT  CONFLICT 171 171
FT  CONFLICT 195 195
FT  CONFLICT 248 248
FT  CONFLICT 264 264
FT  CONFLICT 277 277
FT  CONFLICT 348 348
FT  CONFLICT 349 349
FT  CONFLICT 380 380
FT  CONFLICT 395 395
FT  CONFLICT 412 412
FT  CONFLICT 477 477
FT  CONFLICT 513 513
FT  CONFLICT 515 515
FT  CONFLICT 545 545
FT  CONFLICT 551 551
FT  CONFLICT 556 556
FT  CONFLICT 564 564
FT  CONFLICT 570 570
FT  CONFLICT 583 583
FT  CONFLICT 591 591
FT  CONFLICT 591 591
FT  CONFLICT 619 619
FT  CONFLICT 664 664
FT  CONFLICT 679 680
FT  CONFLICT 690 690
Query Match 74.7%; Score 68; DB 1; Length 1147;
Best Local Similarity 72.2%; Pred. No. 0.0048;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 NNNVEKAPSATSSPVTTQD 18
||||| | | | |

```

```

Db 25 NNNVEKTPGAIPSTTQD 42
RESULT 3
NS2D_HUMAN
ID NS2D_HUMAN STANDARD; PRT; 1147 AA.
AC O60591; O60604;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE NITRIC OXIDE SYNTHASE, INDUCIBLE IID (EC 1.14.13.39) (NOS, TYPE II D)
DE (INDUCIBLE NOS) (INOS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle, and Heart muscle;
RX MEDLINE=99066690; PubMed=9851365;
RA Adams V., Krabbes S., Jiang H., Yu J., Rahmel A., Gielen S.,
RT Schuler G., Hambrecht R.;
RT "Complete coding sequence of inducible nitric oxide synthase from
RT human heart and skeletal muscle of patients with chronic heart
RT failure."
RL Nitric Oxide 2:242-249(1998).
CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO
CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS. MAY BE INVOLVED IN
CC THE PATHOGENESIS OF DILATED CARDIOMYOPATHY OR OF EXERCISE
CC INTOLERANCE OBSERVED IN PATIENTS WITH CHRONIC HEART FAILURE.
CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + H+ -> CITRULLINE +
CC NITRIC OXIDE + N NADP(+).
CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME (BY SIMILARITY).
CC -!- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (BY
CC SIMILARITY).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE HEART AND SKELETAL MUSCLE
CC DURING CHRONIC HEART FAILURE, BUT NOT IN HEALTHY INDIVIDUALS.
CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF049656; AAC83553.1; -
DR EMBL; AF051164; AAC83554.1; -
DR HSP; P29477; INOC.
DR InterPro; IPR001094; -
DR InterPro; IPR001433; -
DR InterPro; IPR001709; -
DR InterPro; IPR003097; -
DR Pfam; PF00667; FAD_binding; 1.
DR Pfam; PF00175; oxidored_fad; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KW Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;
KW Heme; Zinc; Metal-binding; Multigene family.
FT BINDING 197 197
FT DOMAIN 506 526
FT NP_BIND 620 651
FT NP_BIND 764 775
FT NP_BIND 900 910
FT NP_BIND 975 993
FT NP_BIND 1073 1088
FT METAL 107 107
FT METAL 112 112
FT CONFLICT 10 10
FT CONFLICT 72 72
FT CONFLICT 107 107
FT CONFLICT 128 128
FT CONFLICT 130 130
FT CONFLICT 171 171
FT CONFLICT 195 195
FT CONFLICT 248 248
FT CONFLICT 264 264
FT CONFLICT 277 277
FT CONFLICT 348 348
FT CONFLICT 349 349
FT CONFLICT 380 380
FT CONFLICT 395 395
FT CONFLICT 412 412
FT CONFLICT 477 477
FT CONFLICT 513 513
FT CONFLICT 515 515
FT CONFLICT 545 545
FT CONFLICT 551 551
FT CONFLICT 556 556
FT CONFLICT 564 564
FT CONFLICT 570 570
FT CONFLICT 583 583
FT CONFLICT 591 591
FT CONFLICT 591 591
FT CONFLICT 619 619
FT CONFLICT 664 664
FT CONFLICT 679 680
FT CONFLICT 690 690

```

FT CONFLICT 248 248 N -> S (IN AAC83554).  
 FT CONFLICT 271 271 D -> A (IN AAC83554).  
 FT CONFLICT 399 399 G -> E (IN AAC83554).  
 FT CONFLICT 640 640 P -> Q (IN AAC83554).  
 FT CONFLICT 731 731 A -> T (IN AAC83554).  
 FT CONFLICT 937 937 H -> N (IN AAC83554).  
 FT CONFLICT 1008 1009 TL -> NF (IN AAC83554).  
 FT CONFLICT 1024 1024 E -> K (IN AAC83554).  
 FT CONFLICT 1076 1076 I -> L (IN AAC83554).  
 FT CONFLICT 1129 1129 F -> V (IN AAC83554).  
 SQ SEQUENCE 1147 AA; 130528 MW; FF7E4C7ABA76D820 CRC64;

Query Match 74.7%; Score 68; DB 1; Length 1147;

Best Local Similarity 72.2%; Pred. No. 0.0048; 5; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPTQD 18

DB 25 NNNVEKTPGAIPSTTQD 42

RESULT 4

NOS2\_MACMU STANDARD; PRT; 162 AA.

AC 046650; (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)

DE (INDUCIBLE NOS) (INOS) (FRAGMENT).

GN NOS2.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

OX NCBI\_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Microglia;

RX MEDLINE=97056192; PubMed=8900532;

RA Lane T.E., Buchmeier M.J., Watry D.D., Fox H.S.;

RT "Expression of inflammatory cytokines and inducible nitric oxide

synthase in brains of HIV-infected rhesus monkeys: applications to

HIV-induced central nervous system disease.";

RL Mol. Med. 2:27-37(1996).

CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE

WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. INOS AND NO MAY

CONTRIBUTE TO SIMILAN IMMUNODEFICIENCY VIRUS (SIV)-INDUCED CENTRAL

NERVOUS SYSTEM DISEASE.

CC -1- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +

NITRIC OXIDE + N NADP(+).

CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES

TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF

THE ENZYME (BY SIMILARITY).

CC -1- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY

SIMILARITY).

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- INDUCTION: BY LIPOPOLYSACCHARIDES.

CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.

-----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----

CC EMBL; U31907; AAC39525.1; -.

DR HSP; P29477; INOC.

KW Oxidoreductase; NADPH; FAD; FMN; Calmodulin-binding; Heme;

Multigene family.

FT NON\_TER 1 1  
 FT NON\_TER 162 162  
 SQ SEQUENCE 162 AA; 17813 MW; 0457464D32287065 CRC64;

Query Match 71.4%; Score 65; DB 1; Length 162;

Best Local Similarity 77.8%; Pred. No. 0.0016;

Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPTQD 18

DB 5 NNNMEKAACATSSSLVTQD 22

RESULT 5

NOS2\_MOUSE STANDARD; PRT; 1144 AA.

AC P29477; 070515; 070516;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE NITRIC OXIDE SYNTHASE, INDUCIBLE (EC 1.14.13.39) (NOS, TYPE II)

DE (INDUCIBLE NOS) (INOS) (MACROPHAGE NOS) (MAC-NOS).

GN NOS2 OR INOSL.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92229444; PubMed=1373522;

RA Xie Q.-W., Cho H.J., Calaycay J., Mumford R.A., Swiderek K.M.,

RA Lee T.D., Ding A., Troso T., Nathan C.;

RT "Cloning and characterization of inducible nitric oxide synthase from

mouse macrophages.";

RL Science 256:225-228(1992).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=92357701; PubMed=1379716;

RA Lowenstein C.J., Glatt C.S., Bredt D.S., Snyder S.H.;

RT "Cloned and expressed macrophage nitric oxide synthase contrasts with

the brain enzyme.";

RL Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=92210618; PubMed=1372907;

RA Lyons C.R., Orloff G.J., Cunningham J.M.;

RT "Molecular cloning and functional expression of an inducible nitric

oxide synthase from a murine macrophage cell line.";

RL J. Biol. Chem. 267:6370-6374(1992).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=96088781; PubMed=7503239;

RA Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.;

RT "Role of NF-kappa B in the regulation of inducible nitric oxide

synthase in an MTL cell line.";

RL Am. J. Physiol. 269:F718-F729(1995).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=DBA/2J, BALB/CBYJ, SJL/J, NOD/LTJ, AND B10.S/J; TISSUE=Spleen;

RA Ma R.Z., Teuscher C.;

RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF I16-496.

RX MEDLINE=97477482; PubMed=9334294;

RA Crane B.R., Arvai A.S., Gachhui R., Wu C., Ghosh D.K., Getzoff E.D.,

RA Stuehr D.J., Tainer J.A.;

RT "The structure of nitric oxide synthase oxygenase domain and

inhibitor complexes.";

RL Science 278:425-431(1997).

RN [7]

RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.

RX MEDLINE=20031637; PubMed=10562538;

RA Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C.,  
RA Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.;  
RT "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin  
hook and pterin-binding segment in dimerization and  
tetrahydrobiopterin interaction.";  
EMBO J. 18:6260-6270(1999).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.  
RX MEDLINE=98182450; PubMed=95161116;  
RA Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,  
RA Tainer J.A.;  
RT "Structure of nitric oxide synthase oxygenase dimer with pterin and  
substrate.";  
Science 279:2121-2126(1998).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.  
RX MEDLINE=20031638; PubMed=10562539;  
RA Crane B.R., Rosenfeld R.J., Arvai A.S., Ghosh D.K., Ghosh S.,  
RA Tainer J.A., Stuehr D.J., Getzoff E.D.;  
RT "N-terminal domain swapping and metal ion binding in nitric oxide  
synthase dimerization.";  
EMBO J. 18:6271-6281(1999).  
RN [10]  
RP EFFECT OF ASPIRIN.  
RC TISSUE-Macrophage;  
RX MEDLINE=95372392; PubMed=7544010;  
RA Amin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,  
RA Weissmann G., Abramson S.B.;  
RT "The mode of action of aspirin-like drugs: effect on inducible nitric  
oxide synthase.";  
Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).  
CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO  
MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.  
CC -!- CATALYTIC ACTIVITY: L-ARGININE + N NADPH + M O(2) = CITRULLINE +  
NITRIC OXIDE + N NADP(+).  
CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
THE ENZYME.  
CC -!- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN  
INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE  
EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL  
MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY.  
CC -!- SUBUNIT: HOMODIMER.  
CC -!- TISSUE SPECIFICITY: MACROPHAGES.  
CC -!- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES.  
CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL; M87039; AAA39315.1; -  
DR EMBL; M92649; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; M84373; AAA39834.1; -  
DR EMBL; U43428; AAC52356.1; -  
DR EMBL; AF065919; AAC17914.1; -  
DR EMBL; AF065920; AAC17915.1; -  
DR EMBL; AF065921; AAC17916.2; -  
DR EMBL; AF065922; AAC17917.1; ALT\_INIT.  
DR EMBL; AF065923; AAC17918.2; -  
DR PIR; A43271; A43271.  
DR PIR; A42166; A42166.  
DR PDB; 1NOC; 18-NOV-98.  
DR PDB; 1NOS; 18-NOV-98.  
DR PDB; 2NOS; 18-NOV-98.  
DR PDB; 1NOD; 23-MAR-99.  
DR PDB; 2NOD; 23-MAR-99.  
DR PDB; 3NOD; 23-MAR-99.

DR PDB; 1DF1; 08-DEC-99.  
DR PDB; 1DW; 04-FEB-00.  
DR PDB; 1DMW; 06-FEB-00.  
DR PDB; 1DMW; 06-FEB-00.  
DR PDB; 1QOM; 15-DEC-99.  
DR PDB; 1DD7; 29-MAR-00.  
DR MGD; MGI:97361; Nos2.  
DR InterPro; IPR001094; -  
DR InterPro; IPR001433; -  
DR InterPro; IPR001709; -  
DR InterPro; IPR003097; -  
DR Pfam; PF00667; FAD\_binding; 1.  
DR Pfam; PF00175; oxidored\_fad; 1.  
DR PRINTS; PR00369; FLAVODOXIN.  
DR PRINTS; PR00371; FPNCR.  
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;  
KW Zinc; Metal-binding; Multigene family; 3D-structure.  
FT BINDING 194 194  
FT DOMAIN 503 523  
FT NP\_BIND 617 648  
FT NP\_BIND 761 772  
FT NP\_BIND 897 907  
FT NP\_BIND 972 990  
FT NP\_BIND 1070 1085  
FT METAL 104 104  
FT METAL 109 109  
FT VARIANT 211 211  
FT VARIANT 967 967  
FT VARIANT 968 968  
FT CONFLICT 19 19  
FT CONFLICT 191 191  
FT CONFLICT 844 844  
FT SEQUENCE 1144 AA; 130574 MW; 0735BE676113457F CRC64;  
QY 1 NNVKAPSPVPTQD 18  
DB 25 NNVKTPCAVLSPTQD 42  
Query Match 62.6%; Score 57; DB 1; Length 1144;  
Best Local Similarity 61.1%; Pred. No. 0.27;  
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
-----  
RESULT 6  
ALS3\_CANAL STANDARD; PRT; 1119 AA.  
AC 074623;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE AGGLUTININ-LIKE PROTEIN 3 PRECURSOR.  
GN ALS3.  
OS Candida albicans (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5476;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN:1161;  
RX MEDLINE=98309840; PubMed=9644209;  
RT Hoyer L.L., Payne T.L., Bell M., Myers A.M., Scherer S.;  
RT "Candida albicans ALS3 and insights into the nature of the ALS gene  
family";  
RL Curr. Genet. 33:451-459(1998).  
CC -!- FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.  
CC -!- PTM: N-GLYCOSYLATED AND O-GLYCOSYLATED (POTENTIAL).  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial



CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>;  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; U07956; AAC39486.1; -.  
KW Cell adhesion; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 17  
FT CHAIN 18 1119  
FT DOMAIN 433 792  
FT REPEAT 433 468  
FT REPEAT 433 468  
FT REPEAT 469 504  
FT REPEAT 505 540  
FT REPEAT 541 576  
FT REPEAT 577 612  
FT REPEAT 613 648  
FT REPEAT 649 684  
FT REPEAT 685 720  
FT REPEAT 721 756  
FT REPEAT 757 792  
FT DOMAIN 399 404  
FT DOMAIN 450 455  
FT DOMAIN 557 563  
FT DOMAIN 593 597  
FT DOMAIN 630 635  
FT DOMAIN 666 671  
FT DOMAIN 702 707  
FT DOMAIN 738 743  
FT DOMAIN 774 777  
FT DOMAIN 1044 1047  
FT CARBOHYD 471 471  
FT CARBOHYD 543 543  
FT CARBOHYD 579 579  
FT CARBOHYD 651 651  
FT CARBOHYD 687 687  
FT CARBOHYD 723 723  
FT CARBOHYD 759 759  
FT CARBOHYD 845 845  
FT CARBOHYD 987 987  
FT CARBOHYD 1050 1050  
FT CARBOHYD 1061 1061  
SQ SEQUENCE 1119 AA; 119927 MW; 6A3FB3FC879A71 CRC64;

Query Match 59.3%; Score 54; DB 1; Length 1119;  
Best Local Similarity 75.0%; Pred. No. 0.79;  
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 NNVEKAPSATSSPVT 16  
|| |||||  
DB 1029 NNGGKAPSATSSPST 1044

RESULT 7  
MERE\_PSEAE STANDARD; PRT; 78 AA.  
AC P06690;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 01-OCT-1989 (Rel. 12, Last annotation update)  
DE HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERE.  
GN MERE.  
OS Pseudomonas aeruginosa.  
OG Plasmid pVSI.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TRANSPOSON-rn501;  
RX MEDLINE=86174347; PubMed=3007931;  
RA Brown N.L., Misra T.K., Winnie J.W., Schmidt A., Sieff M., Silver S.;  
RT "The nucleotide sequence of the mercuric resistance operons of  
RT plasmid R100 and transposon Tn501; further evidence for mer genes  
RT which enhance the activity of the mercuric ion detoxification

RT system.";  
RL Mol. Gen. Genet. 202:143-151(1986).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; Z00027; CAA77325.1; -.  
KW Mercuric resistance; Hypothetical protein; Transposable element;  
KW Plasmid.  
SQ SEQUENCE 78 AA; 8410 MW; EIEF23E690CF115D CRC64;

Query Match 49.5%; Score 45; DB 1; Length 78;  
Best Local Similarity 53.3%; Pred. No. 1.1;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 NNVEKAPSATSSPVT 16  
|| || || || ||  
DB 2 NNPERLPSETHKPT 16

RESULT 8  
HBL1\_CAEEL STANDARD; PRT; 982 AA.  
ID HBL1\_CAEEL  
AC Q9XVD3; Q19389;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE HUNCHBACK-LIKE PROTEIN.  
GN HBL-1 OR F13D11.2.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Telodermidae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RX MEDLINE=99117349; PubMed=9917360;  
RA Fay D.S., Stanley H.M., Han M., Wood W.B.;  
RT "A Caenorhabditis elegans homologue of hunchback is required for late  
RT stages of development but not early embryonic patterning.";  
RL Dev. Biol. 205:240-253(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Fulton L.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: REQUIRED FOR LATE STAGES OF DEVELOPMENT.  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE)  
CC -!- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN ECTODERMAL CELLS DURING  
CC EMBRYONIC AND LARVAL DEVELOPMENT.  
CC -!- SIMILARITY: BELONGS TO THE HUNCHBACK FAMILY OF C2H2-TYPE ZINC-  
CC FINGER PROTEINS.

-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; AF097737; AAD16170.1; -.  
DR EMBL; U40939; AAA81701.2; ALT\_INIT.  
DR WormPep; F13D11.2; CE23646.  
DR InterPro; IPR000822; -.  
DR Pfam; PF00096; zf-C2H2; 9.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 3.

RESULT 11

```

FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 619 619 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 677 AA; 74432 MW; 3D22C37CF856F8BA CRC64;

Query Match 47.8%; Score 43.5; DB 1; Length 677;
Best Local Similarity 39.1%; Pred. No. 21;
Matches 9; Conservative 5; Mismatches 4; Indels 5; Gaps 1;

Oy 1 NNNVEK-----APSATSPVTQD 18
   ||: | : ||: |||
Db 435 NNSAQSPQTKTTPATTPMTQD 457

RESULT 12
VGP_EBORS
ID VGP_EBORS STANDARD; PRT; 677 AA.
AC Q89853;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE STRUCTURAL GLYCOPROTEIN PRECURSOR (VIRION SPIKE GLYCOPROTEIN)
[CONTAINS: GP1; GP2].
GN GP.
OS Ebola virus (strain Reston Siena/Philippine-92) (Ebov).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
OC Filovirus.
OX NCBI_Taxid=129004;
RN NCBI
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96195018; Pubmed=8622982;
RA Sanchez A., Trappier S.G., Mahy B.W.J., Peters C.J., Nichol S.T.;
RT "The virion glycoproteins of Ebola viruses are encoded in two reading
frames and are expressed through transcriptional editing.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:3602-3607(1996).
CC -!- FUNCTION: STRUCTURAL PROTEIN THAT FORMS THE VIRION SPIKE AND WHICH
IS RESPONSIBLE FOR BINDING TO TARGET CELLS AND SUBSEQUENT FUSION
OF THE VIRAL AND HOST-CELL MEMBRANES.
CC -!- SUBUNIT: HOMOTRIMER; EACH MONOMER CONSIST OF A GP1 AND A GP2
SUBUNIT LINKED BY DISULFIDE BONDS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. GP1 CAN ALSO BE
SHED BY THE VIRUS AFTER PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -!- PTM: N-GLYCOSYLATED, COULD ALSO BE O-GLYCOSYLATED (BY SIMILARITY).
CC -!- PTM: PROCESSING INTO GP1 AND GP2 IS EFFECTED BY THE HOST FURIN (BY
SIMILARITY).
CC -!- MISCELLANEOUS: THE FULL-LENGTH GLYCOPROTEIN IS SYNTHESIZED AS A
RESULT OF RNA EDITING, AN ADDITIONAL A RESIDUE IS INSERTED DURING
TRANSCRIPTION. WITHOUT RNA-EDITING, A SMALL GLYCOPROTEIN (SGP) IS
PRODUCED.
CC -!- SIMILARITY: BELONGS TO THE FILOVIRUSES GLYCOPROTEIN FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
CC EMBL; U23417; AAC54891.1; -
CC EMBL; U23416; AAC54889.1; -
CC InterPro: IPR002561; -
DR Pfam; PF01611; Filo_glycop: 1.
KW Transmembrane; Envelope protein; Glycoprotein; Signal; RNA editing.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 677 STRUCTURAL GLYCOPROTEIN.
FT CHAIN 503 502 GP1.
FT CHAIN 503 677 GP2.
FT DOMAIN 33 650 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 651 677 POTENTIAL.
FT DOMAIN 674 677 CYTOPLASMIC (POTENTIAL).

```

```

FT DISULFID 602 609 BY SIMILARITY.
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 420 420 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 619 619 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 677 AA; 74523 MW; DA9770A7BAFED9BD CRC64;

Query Match 47.8%; Score 43.5; DB 1; Length 677;
Best Local Similarity 39.1%; Pred. No. 21;
Matches 9; Conservative 5; Mismatches 4; Indels 5; Gaps 1;

QY 1 NNNVEK-----APSATSSPVTD 18
||: : : :||:|
Db 435 NNSAQSPQTKTTPAPTASPTQD 457

RESULT 13
BRC2_MOUSE
AC BRC2_MOUSE STANDARD; PRT; 3329 AA.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BREAST CANCER TYPE 2 SUSCEPTIBILITY PROTEIN.
GN BRCA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=972117789; PubMed=9063750;
RA Connor F., Smith A., Wooster R., Stratton M., Dixon A., Campbell E.,
RA Tait T.M., Freeman T., Ashworth A.;
RT "Cloning, chromosomal mapping and expression pattern of the mouse
RT Brca2 gene.";
RL Hum. Mol. Genet. 6:291-300(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=97237041; PubMed=9119389;
RA Sharan S.K., Bradley A.;
RT "Murine Brca2: sequence, map position, and expression pattern.";
RL Genomics 40:234-241(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=97384941; PubMed=9242436;
RA McAllister K.A., Haugen-Strano A., Hagevik S., Brownlee H.A.,
RA Collins N.K., Futreal P.A., Bennett L.M., Wiseman R.W.;
RT "Characterization of the rat and mouse homologues of the BRCA2 breast
RT cancer susceptibility gene.";
RL Cancer Res. 57:3121-3125(1997).
RN [4]
RP SEQUENCE OF 18-200 FROM N.A.
RX MEDLINE=97075121; PubMed=8917547;
RA Rajan J.V., Wang M., Marquis S.T., Chodosh L.A.;
RT "Brca2 is coordinately regulated with Brca1 during proliferation and
RT differentiation in mammary epithelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13078-13083(1996).

```

---

```

RN [5]
RX SEQUENCE OF 569-625 FROM N.A.
RX MEDLINE=97341126; PubMed=9196008;
RA McAllister K.A., Ramachandran S., Haugen-Strano A., Fiedorek F.T. Jr.,
RA Wiseman R.W.;
RT "Genetic mapping of the Brca2 breast cancer susceptibility gene on
RT mouse chromosome 5.";
RL Mamm. Genome 8:540-541(1997).
CC -1- FUNCTION: MAY PARTICIPATE IN A PATHWAY ASSOCIATED WITH THE
CC ACTIVATION OF DOUBLE-STRAND BREAK REPAIR AND/OR HOMOLOGOUS
CC RECOMBINATION (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH RAD51 (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN
CC CEREBELLUM, TESTIS, ILEUM, APPENDIX, EPIDYMISS, OVARY AND MAMMARY
CC GLAND. NO EXPRESSION IN LUNG.
CC -1- DEVELOPMENTAL STAGE: IN THE MAMMARY GLAND, EXPRESSION INCREASES
CC DRAOMATICALLY DURING PREGNANCY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U82270; AAB48306.1; -
CC EMBL; U72947; AAB40720.1; -
CC EMBL; U65594; AAC23702.1; -
CC EMBL; U89652; AAB71377.1; -
CC EMBL; U89503; AAC53276.1; -
CC MGD; MGI:109337; Brca2.
DR InterPro; IPR002093; -
DR Pfam; PF00634; BRCA2_repeat; 7.
DR PROSITE; PS50138; BRCA2_REPEAT; 6.
KW Polymorphism; Repeat.
FT DOMAIN 981 2038 7 X 34 AA APPROXIMATE BRCA2 REPEATS.
FT REPEAT 981 1015 BRCA2 1.
FT REPEAT 1192 1226 BRCA2 2.
FT REPEAT 1394 1428 BRCA2 3.
FT REPEAT 1491 1525 BRCA2 4.
FT REPEAT 1623 1657 BRCA2 5.
FT REPEAT 1924 1958 BRCA2 6.
FT REPEAT 2004 2038 BRCA2 7.
FT VARIANT 44 44 S -> F (IN STRAINS C57BL/6 AND 129/SV).
FT VARIANT 340 340 T -> P (IN STRAIN 129/SV).
FT VARIANT 377 377 N -> H (IN STRAIN C57BL/6).
FT VARIANT 407 407 H -> P (IN STRAIN C57BL/6).
FT VARIANT 661 661 I -> V (IN STRAIN C57BL/6).
FT VARIANT 739 739 P -> H (IN STRAIN C57BL/6).
FT VARIANT 1038 1038 I -> L (IN STRAINS C57BL/6 AND 129/SV).
FT VARIANT 1198 1199 GF -> RI (IN STRAIN C57BL/6).
FT VARIANT 1257 1257 Q -> P (IN STRAIN C57BL/6).
FT VARIANT 1392 1392 Q -> R (IN STRAIN C57BL/6).
FT VARIANT 1520 1521 FD -> CG (IN STRAIN C57BL/6).
FT VARIANT 1583 1583 R -> W (IN STRAIN C57BL/6).
FT VARIANT 1613 1613 C -> W (IN STRAIN C57BL/6).
FT VARIANT 1686 1686 S -> R (IN STRAIN C57BL/6).
FT VARIANT 1799 1799 S -> F (IN STRAIN 129/SV).
FT VARIANT 1881 1881 P -> L (IN STRAIN C57BL/6).
FT VARIANT 1894 1894 S -> F (IN STRAIN 129/SV).
FT VARIANT 2141 2141 Q -> K (IN STRAIN C57BL/6).
FT VARIANT 2392 2392 S -> R (IN STRAIN C57BL/6).
FT VARIANT 2605 2605 K -> Q (IN STRAIN C57BL/6).
FT VARIANT 2648 2648 R -> P (IN STRAIN C57BL/6).
FT VARIANT 2717 2717 R -> C (IN STRAIN 129/SV).
FT VARIANT 2729 2729 L -> M (IN STRAIN 129/SV).
FT VARIANT 2814 2814 Q -> H (IN STRAIN C57BL/6).
FT VARIANT 2827 2827 A -> P (IN STRAIN C57BL/6).
FT VARIANT 2907 2907 S -> I (IN STRAIN 129/SV).
FT VARIANT 2929 2929 H -> L (IN STRAIN 129/SV).
FT VARIANT 3058 3058 A -> G (IN STRAIN C57BL/6).
FT VARIANT 3071 3071 A -> G (IN STRAIN C57BL/6).

```

FT	SIGNAL	1	13	POTENTIAL.
FT	CHAIN	14	438	LIN-3 PROTEIN.
FT	DOMAIN	14	230	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	231	253	POTENTIAL.
FT	DOMAIN	254	438	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	150	194	EGF-LIKE.
FT	DISULFID	154	164	BY SIMILARITY.
FT	DISULFID	158	182	BY SIMILARITY.
FT	DISULFID	184	193	BY SIMILARITY.
FT	CARBOHYD	161	161	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	211	225	MISSING (LN SHORT ISOFORM).
FT	CONFLICT	19	20	MISSING (LN REF. 2).
SEQ	SEQUENCE	438 AA;	48923 MW;	3434C779D8B54501 CRC64;

  

Query Match		46.2%;	Score 42;	DB 1;	Length 438;
Best Local Similarity		53.3%;	Pred. No. 23;		
Matches	8; Conservative	3;	Mismatches	4;	Indels 0; Gaps 0;

  

Qy	2 NNVEKAPSATSSPVT 16
I :	I
Db	63 NEIGDAPSTSPET 77

  

```

RESULT 15
YS45_CAEEL          STANDARD;      PRT;    428 AA.
ID YS45_CAEEL
AC Q09660;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DE PUTATIVE CYTOCHROME P450 CYP44 (EC 1.14.-.-).
GN CYP44 OR ZK177.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
OC Rhabditiidae; Peloderiinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Anderson K.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBDJ databases.
CC -! FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -! SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@lsb-sib.ch).
CC -----
CC EMBL; U21321; AAB36969.1; -.
CC WormPep; ZKI77.5; CE02094.
CC InterPro; IPR001128; -.
CC Pfam; PF00067; p450; 2.
CC PROSITE; PS00086; CYTOCHROME_P450; 1.
CC KW Hypothetical protein; Oxidoreductase; Monooxygenase; Heme.
FT BINDING 377 377 HEME (BY SIMILARITY).
FT BLASTING 377 377
SQ SEQUENCE 428 AA; 49015 MW; 71DFB8B35FEE7A1 CRC64;

```

  

Qy	3 NVEKAP-SATSSPVT 16
I	
Db	11 NVEKCPSPTSSPNT 25

  

Query Match		45.6%;	Score 41.5;	DB 1;	Length 428;
Best Local Similarity		73.3%;	Pred. No. 27;		
Matches	11; Conservative	0;	Mismatches	3;	Indels 1; Gaps 1;

Search completed: September 10, 2001, 14:09:55  
Job time: 564 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:01:15 ; Search time 42.28 Seconds  
(without alignments)  
32.430 Million cell updates/sec

Title: US-08-833-506C-32  
Perfect score: 91  
Sequence: 1 NNVKRAPSTSSPVTQD 18  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	94.5	1153	2 A49676	nitric-oxide synth
2	68	74.7	1147	1 S47647	nitric-oxide synth
3	68	74.7	1147	1 I56575	nitric-oxide synth
4	68	74.7	1147	1 S38253	nitric-oxide synth
5	68	74.7	1147	1 I53165	nitric-oxide synth
6	68	74.7	1147	2 J55027	nitric-oxide synth
7	68	74.7	1147	2 J55028	nitric-oxide synth
8	68	74.7	1147	2 J55029	nitric-oxide synth
9	57	62.6	1144	1 A43271	nitric-oxide synth
10	55	60.4	1147	2 S65440	nitric-oxide synth
11	47	51.6	758	2 S65169	hypothetical prote
12	46	50.5	246	2 S74559	peptidyl-prolyl ci
13	46	50.5	394	2 T26968	hypothetical prote
14	44	48.4	908	2 T16057	hunchback-related
15	44	48.4	982	2 T43676	protein kinase cek
16	44	48.4	1338	2 T40993	BPLF1 protein - hu
17	44	48.4	3149	1 Q0BE8	breast cancer tumo
18	43.5	47.8	3328	2 T30835	breast cancer susc
19	43.5	47.8	3329	2 T42205	breast cancer tumo
20	43.5	47.8	3329	2 T30904	probable iron (III
21	43	47.3	349	2 A75169	internalin- relate
22	43	47.3	1045	2 T41119	hypothetical prote
23	42	46.2	366	2 T24546	lin-3 protein prec
24	42	46.2	438	2 S8263	hypothetical prote
25	42	46.2	639	2 T20772	hypothetical prote
26	41.5	45.6	428	2 T27763	hypothetical prote
27	41.5	45.6	767	1 C02PCD	cdc10 start contro
28	41	45.1	236	2 PC4396	mucin 3 T9 - human
29	41	45.1	327	2 T38261	hypothetical prote

30	41	45.1	347	2 S44995	pectate lyase - Er
31	41	45.1	474	2 T45818	hypothetical prote
32	41	45.1	492	2 T28025	hypothetical prote
33	41	45.1	509	2 T31706	hypothetical prote
34	41	45.1	545	2 T43513	Hsk1 protein kinas
35	41	45.1	581	2 S53105	pectinesterase pre
36	41	45.1	662	2 T18233	probable transcrip
37	41	45.1	1011	2 T20785	hypothetical prote
38	41	45.1	1132	2 C75259	probable iron-sulf
39	41	45.1	2586	2 T21676	hypothetical prote
40	41	45.1	4549	2 T20771	hypothetical prote
41	41	45.1	4667	2 T20774	hypothetical prote
42	40.5	44.5	727	2 T29612	hypothetical prote
43	40.5	44.5	753	2 D81219	NADH dehydrogenase
44	40.5	44.5	993	2 A38437	probable homeotic
45	40	44.0	78	2 S70148	merE protein - Xan

## ALIGNMENTS

RESULT 1

A49676  
nitric-oxide synthase (EC 1.14.13.39), inducible - human  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 20-Jun-2000  
C:Accession: A49676; JX0345; G01947; I38933; S47366; A47475  
R:Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; Hall, V.S.;  
Proc. Natl. Acad. Sci. U.S.A. 90, 11419-11423, 1993  
A:Title: Cloning, characterization, and expression of a cDNA encoding an inducible ni  
A:Reference number: A49676; MUID:94068614  
A:Accession: A49676  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1153 <RES>  
A:Cross-references: EMBL:X73029; NID:g441452; PIDN:CAA51512.1; PID:g441453  
R:Hokari, A.; Zeniya, M.; Esumi, H.  
J. Biochem. 116, 575-581, 1994  
A:Title: Cloning and functional expression of human inducible nitric oxide synthase (  
A:Reference number: JX0345; MUID:95155267  
A:Accession: JX0345  
A:Molecule type: mRNA  
A:Residues: 1-607, 'L', 609-1153 <HOK>  
A:Cross-references: DBJ:D26525; NID:g559326; PIDN:BAA05531.1; PID:g1228940  
A:Experimental source: glioblastoma cell line A-172  
R:Park, C.; Park, R.; Krishna, G.  
submitted to the EMBL Data Library, July 1995  
A:Reference number: G08912  
A:Accession: G01947  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-607, 'L', 609-1153 <PAR>  
A:Cross-references: EMBL:U31511; NID:g951320; PIDN:AAB43041.1; PID:g951321  
R:Guo, F.H.; De Raeve, H.R.; Rice, T.W.; Stuehr, D.J.; Thunnissen, F.B.; Erzurum, S.C  
Proc. Natl. Acad. Sci. U.S.A. 92, 7809-7813, 1995  
A:Title: Continuous nitric oxide synthesis by inducible nitric oxide synthase in norm  
A:Reference number: I38933; MUID:95372368  
A:Accession: I38933  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-675, 'I', 677-932, 'G', 934-965, 'A', 967-1153 <RE2>  
A:Cross-references: EMBL:U20141; NID:g687680; PIDN:AAB60366.1; PID:g687681  
R:Maier, R.; Bilbe, G.; Rediske, J.; Lotz, M.  
Biochim. Biophys. Acta 1208, 145-150, 1994  
A:Title: Inducible nitric oxide synthase from human articular chondrocytes: cDNA clon  
A:Reference number: S47566; MUID:94368816  
A:Accession: S47566  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-22, 'G', 24-153, 'L', 155-176, 'V', 178-799, 'A', 801-912, 'P', 914-1153 <NAI>  
A:Cross-references: EMBL:U05810; NID:g452487; PIDN:AAA5666.1; PID:g452488  
R:Geller, D.A.; Lovenstein, C.J.; Shapiro, R.A.; Nussler, A.K.; Di Silvio, M.; Wang,  
Proc. Natl. Acad. Sci. U.S.A. 90, 3491-3495, 1993

Db 25 NNNVEKTPCAIPSPVTQD 42

RESULT 3

156575

nitric-oxide synthase (EC 1.14.13.39) [similarity] - rat

A:Reference number: A47475; MUID:93234523

A:Accession: A47475

A>Status: Preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-422,'I',424-804,'D',806-830,'SP',833-932,'G',934-965,'A',967-986,'V',988-1000

A:Cross-references: GB:L09210; NID:g292241; PIDN:AAA59171.1; PID:g292242

A:Experimental source: hepatocytes

A>Note: sequence extracted from NCBI backbone (NCBIP:129733)

C:Genetics:

A:Gene: GDB:NOS2A; NOS2; INOS

A:Cross-references: GDB:L39215; OMIM:163730

A:Map position: 17cen-17q11.2

C:Function:

A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrithemoprotein reductase

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal

F:509-539/Region: calmodulin binding #status predicted

F:539-1127/Domain: NADPH--ferrithemoprotein reductase homology <FEH>

F:541-677/Domain: flavodoxin homology <FLX>

F:623-654/Region: FMN binding #status predicted

F:763-778/Region: FAD-pyrophosphate binding #status predicted

F:903-913/Region: FAD-isalloxazine binding #status predicted

F:978-996/Region: NADP-ribose binding #status predicted

F:1076-1091/Region: NADP-adenine binding #status predicted

F:200/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 94.5%; Score 86; DB 2; Length 1153;

Best Local Similarity 94.4%; Pred. No. 1.3e-05;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18

||||||| |||||||

Db 25 NNNVEKAPCATSSPVTQD 42

RESULT 2

S47647

nitric-oxide synthase (EC 1.14.13.39) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 16-Jun-2000

C:Accession: S47647; JCI1472

R:Geng, Y.; Almqvist, M.; Hansson, G.K.

Biochim. Biophys. Acta 1218, 421-424, 1994

A:Title: cDNA cloning and expression of inducible nitric oxide synthase from rat vascula

A:Reference number: S47647; MUID:94325351

A:Accession: S47647

A:Molecule type: mRNA

A:Residues: 1-1147 <GEN>

A:Cross-references: EMBL:X76881; NID:9439283; PIDN:CAA54208.1; PID:9439284

R:Nunokawa, Y.; Ishida, N.; Tanaka, S.

Biochem. Biophys. Res. Commun. 191, 89-94, 1993

A:Title: Cloning of inducible nitric oxide synthase in rat vascular smooth muscle cells.

A:Reference number: JCI1472; MUID:93191721

A:Accession: JCI1472

A:Molecule type: DNA

A:Residues: 1-71,'Y',73-347,'PV',350-678,'VP',681-720,'L',722-739,'L',741-843,'G',845-1000

A:Cross-references: DBJ:D14051; NID:g286260; PIDN:BAA03138.1; PID:g286261

A:Experimental source: vascular smooth muscle

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrithemoprotein reductase

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal

F:536-1124/Domain: NADPH--ferrithemoprotein reductase homology <FEH>

F:538-674/Domain: flavodoxin homology <FLX>

F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 74.7%; Score 68; DB 1; Length 1147;

Best Local Similarity 72.2%; Pred. No. 0.0099;

Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18

||||||| |||||

Db 25 NNNVEKTPCAIPSPVTQD 42

RESULT 3

156575

nitric-oxide synthase (EC 1.14.13.39) [similarity] - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 05-May-2000

C:Accession: 156575

R:Galea, E.; Reiss, D.J.; Feinstein, D.L.

J. Neurosci. Res. 37, 406-414, 1994

A:Title: Cloning and expression of inducible nitric oxide synthase from rat astrocyte

A:Reference number: 156575; MUID:94231594

A:Accession: 156575

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1147 <RES>

A:Cross-references: EMBL:U03699; NID:9430718; PIDN:AAC13747.1; PID:g430719

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrithemoprotein reductase

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me

F:536-1124/Domain: NADPH--ferrithemoprotein reductase homology <FEH>

F:538-674/Domain: flavodoxin homology <FLX>

F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 74.7%; Score 68; DB 1; Length 1147;

Best Local Similarity 72.2%; Pred. No. 0.0099;

Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18

||||||| |||||

Db 25 NNNVEKTPCAIPSPVTQD 42

RESULT 4

S38253

nitric-oxide synthase (EC 1.14.13.39) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 16-Jun-2000

C:Accession: S38253; JN0457

R:Adachi, H.; Iida, S.; Oguchi, S.; Ohshima, H.; Suzuki, H.; Nagasaki, K.; Kawasaki, E.

Eur. J. Biochem. 217, 37-43, 1993

A:Title: Molecular cloning of a cDNA encoding an inducible calmodulin-dependent nitri

A:Reference number: S38253; MUID:94039059

A:Accession: S38253

A:Molecule type: mRNA

A:Residues: 1-1147 <ADA>

A:Cross-references: GB:D12520; NID:g391858; PIDN:BAA02090.1; PID:g391859

A:Experimental source: liver

R:Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.

Biochem. Biophys. Res. Commun. 191, 767-774, 1993

A:Title: Hepatocytes and macrophages express an identical cytokine inducible nitric o

A:Reference number: JN0457; MUID:93221515

A:Accession: JN0457

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-41,'SS',44-103,105-190,'O',192-213,'R',215-247,'T',249-263,'I',265-373,'S',896-1000,'LG',1003-1015,'RR',1018-1026,'EQ',1029-1147 <QOO>

A:Cross-references: PIDN:AAB26037.1

A:Experimental source: liver

C:Genetics:

A:Gene: NOS

C:Function:

A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NAD

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrithemoprotein re

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me

F:536-1124/Domain: NADPH--ferrithemoprotein reductase homology <FEH>

F:538-674/Domain: flavodoxin homology <FLX>

F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 74.7%; Score 68; DB 1; Length 1147;

Best Local Similarity 72.2%; Pred. No. 0.0099;



Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18  
 ||||| | | | | |  
 Db 25 NNNVEKTPGAIPSPVTQD 42

RESULT 5  
 I53165  
 nitric-oxide synthase (EC 1.14.13.39) [similarity] - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 05-May-2000  
 C:Accession: I53165  
 R:Karlsen, A.E.; Andersen, H.U.; Vissing, H.; Larsen, P.M.; Fey, S.J.; Cuartero, B.G.; M  
 Diabetes 44, 753-758, 1995  
 A:Title: Cloning and expression of cytokine-inducible nitric oxide synthase cDNA from ra  
 A:Reference number: I53165; MUID:95309542  
 A:Accession: I53165  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <RES>  
 A:Cross-references: EMBL:U26686; NID:g886072; PIDN:AAA85861.1; PID:g886073  
 C:Genetics:  
 A:Gene: NOS2  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reduc  
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 74.7%; Score 68; DB 1; Length 1147;  
 Best Local Similarity 72.2%; Pred. No. 0.0099;  
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18  
 ||||| | | | | |  
 Db 25 NNNVEKTPGAIPSPVTQD 42

RESULT 6  
 JC5027  
 nitric-oxide synthase (EC 1.14.13.39) K - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 21-Jan-1997 #sequence\_revision 21-Jan-1997 #text\_change 20-Jun-2000  
 C:Accession: JC5027  
 R:Tsutsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, M  
 Biol. Pharm. Bull. 19, 1374-1376, 1996  
 A:Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and u  
 A:Reference number: JC5027; MUID:97070590  
 A:Accession: JC5027  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <TSU>  
 A:Experimental source: kidney  
 A:Cross-references: DDBJ:D83661; NID:g1209382; PIDN:BAA12035.1; PID:g1853973  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reduc  
 F:191-199/Domain: heme-binding #status predicted <HMB>  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:620-647/Domain: FMN binding #status predicted <FMN>  
 F:764-775,899-910/Domain: FAD binding #status predicted <FAD>  
 F:975-993,1054-1067/Domain: NADP binding #status predicted <NDP>  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 74.7%; Score 68; DB 2; Length 1147;  
 Best Local Similarity 72.2%; Pred. No. 0.0099;  
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18  
 ||||| | | | | |

Db 25 NNNVEKTPGAIPSPVTQD 42

RESULT 7  
 JC5028  
 nitric-oxide synthase (EC 1.14.13.39) L - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 04-Mar-2000  
 C:Accession: JC5028  
 R:Tsutsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa  
 Biol. Pharm. Bull. 19, 1374-1376, 1996  
 A:Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, an  
 A:Reference number: JC5027; MUID:97070590  
 A:Accession: JC5028  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <TSU>  
 A:Experimental source: lung  
 C:Comment: This protein synthesizes nitric oxide from L-arginine.  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein re  
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 74.7%; Score 68; DB 2; Length 1147;  
 Best Local Similarity 72.2%; Pred. No. 0.0099;  
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18  
 ||||| | | | | |  
 Db 25 NNNVEKTPGAIPSPVTQD 42

RESULT 8  
 JC5029  
 nitric-oxide synthase (EC 1.14.13.39) U - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 04-Mar-2000  
 C:Accession: JC5029  
 R:Tsutsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa  
 Biol. Pharm. Bull. 19, 1374-1376, 1996  
 A:Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, an  
 A:Reference number: JC5027; MUID:97070590  
 A:Accession: JC5029  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <TSU>  
 A:Experimental source: uterus  
 C:Comment: This protein synthesizes nitric oxide from L-arginine.  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein re  
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me  
 F:536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F:538-674/Domain: flavodoxin homology <FLX>  
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 74.7%; Score 68; DB 2; Length 1147;  
 Best Local Similarity 72.2%; Pred. No. 0.0099;  
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18  
 ||||| | | | | |  
 Db 25 NNNVEKTPGAIPSPVTQD 42

RESULT 9  
 A43271  
 nitric-oxide synthase (EC 1.14.13.39), calmodulin-independent - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Mar-2000  
 C:Accession: A43271; A42166; JN0458; A46186

R.Xie, Q.; Cho, H.J.; Calaycay, J.; Mumford, R.A.; Swiderex, K.M.; Lee, T.D.; Ding, A.; Science 256, 225-228, 1992  
 A:Title: Cloning and characterization of inducible nitric oxide synthase from mouse macrophages  
 A:Reference number: A43271; MUID:92229444  
 A:Accession: A43271

A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1144 <XIF>  
 A:Cross-references: GB:M87039; NID:q198406; PIDN:AAA39315.1; PID:q198407  
 R.Lyons, C.R.; Orloff, G.J.; Cunningham, J.M.  
 J. Biol. Chem. 267, 6370-6374, 1992

A:Title: Molecular cloning and functional expression of an inducible nitric oxide synthase from mouse macrophages  
 A:Reference number: A42166; MUID:92210618  
 A:Accession: A42166

A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1144 <LYO>  
 A:Cross-references: GB:M84373; NID:g200095; PIDN:AAA39834.1; PID:g200096  
 R.Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.  
 Biochem. Biophys. Res. Commun. 191, 767-774, 1993

A:Title: Hepatocytes and macrophages express an identical cytokine inducible nitric oxide synthase  
 A:Reference number: JN0457; MUID:93221515  
 A:Accession: JN0458

A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-278,'F',280-682,'H',684-937,939-1144 <WOO>  
 A:Experimental source: liver

R.Lowenstein, C.J.; Glatt, C.S.; Bredt, D.S.; Snyder, S.H.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 6711-6715, 1992

A:Title: Cloned and expressed macrophage nitric oxide synthase contrasts with the brain  
 A:Reference number: A46186; MUID:92357701  
 A:Accession: A46186

A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-190,'V',192-765,'P',767-843,'G',845-1144 <LOW>

A:Cross-references: GB:M92649; NID:g200109  
 A:Experimental source: BALB/c, RAW 264.7 cells, macrophage  
 A:Note: sequence extracted from NCBI backbone (NCBIP:113541)

C:Genetics:  
 A:Gene: NOS  
 C:Function:

A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH  
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reductase  
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal

F.533-1121/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F.535-671/Domain: flavodoxin homology <FLX>  
 F.194/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 62.6%; Score 57; DB 1; Length 1144;  
 Best Local Similarity 61.1%; Pred. No. 0.57;  
 Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 NNNVEKAPSATSSPVTD 18  
 Db 25 NNNVKTTCVLSPTIQD 42

RESULT 10  
 S65440  
 nitric-oxide synthase (EC 1.14.13.39) - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 04-Mar-2000  
 C:Accession: S65440

R.Iwashina, M.; Hirata, Y.; Imai, T.; Sato, K.; Marumo, F.  
 Eur. J. Biochem. 237, 668-673, 1996

A:Title: Molecular cloning of endothelial, inducible nitric oxide synthase gene from rat  
 A:Reference number: S65440; MUID:96235231  
 A:Accession: S65440

A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1147 <IWA>

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH--ferrihemoprotein reductase

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; me  
 F.506-535/Region: calmodulin binding  
 F.536-1124/Domain: NADPH--ferrihemoprotein reductase homology <FEH>  
 F.538-674/Domain: flavodoxin homology <FLX>

F.599-618/Region: biopterin binding  
 F.620-647/Region: FMN binding #status predicted  
 F.764-775/Region: FAD binding #status predicted  
 F.901-910/Region: FAD binding #status predicted  
 F.975-993/Region: NADPH binding #status predicted  
 F.1074-1087/Region: NADPH binding #status predicted  
 F.197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 60.4%; Score 55; DB 2; Length 1147;  
 Best Local Similarity 61.1%; Pred. No. 1.2;  
 Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 NNNVEKAPSATSSPVTD 18  
 Db 25 NNNVTTGCAIPSPDQ 42

RESULT 11

S65169  
 hypothetical protein YPL158c - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: hypothetical protein P2570  
 C:Species: Saccharomyces cerevisiae

C:Date: 10-Dec-1994 #sequence\_revision 31-May-1996 #text\_change 05-Dec-1997  
 A:Accession: S65169; S69441  
 R:Purnelle, B.; Coster, F.; Goffeau, A.

submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S65154  
 A:Accession: S65169

A:Molecule type: DNA  
 A:Residues: 1-758 <PUR>

A:Cross-references: EMBL:Z73514; NID:g1370335; PID:e247047; PID:g1370336; MIPS:YPL158  
 A:Experimental source: strain S288C (AB972)  
 R:Purnelle, B.; Comblez, S.; Coster, F.; Naveau, F.; Goffeau, A.

submitted to the EMBL Data Library, March 1996  
 A:Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identifi  
 cally to the human phosphotyrosyl phosphatase activator PTPA and a homologue to the p1

A:Reference number: S69428  
 A:Accession: S69441  
 A:Molecule type: DNA

A:Residues: 1-758 <PUR>  
 A:Cross-references: EMBL:X96770; NID:g1403537; PID:e239043; PID:g1403551  
 C:Genetics:

A:Map position: 16L

Query Match 51.6%; Score 47; DB 2; Length 758;  
 Best Local Similarity 60.0%; Pred. No. 14;  
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 NVEKAPSATSSPVTD 17  
 Db 309 NVQKVPSTATSKTK 323

RESULT 12

S74559  
 peptidyl-prolyl cis-trans isomerase B - Synecocystis sp. (strain PCC 6803)  
 N:Alternate names: hypothetical protein sl10227  
 C:Species: Synecocystis sp.

A:Variety: PCC 6803  
 C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocys

S.

A:Reference number: S74322; MUID:97061201

A:Accession: S74559  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-246 <RAN>  
A:Cross-references: EMBL:D90900; GB:AB001339; NID:g1651768; PIDN:BAAL6711.1; PID:d101744  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Genetics:  
A:Gene: ppiB  
C:Superfamily: cyclophilin homology  
F:63-244/Domain: cyclophilin homology <CYP>

Query Match 50.5%; Score 46; DB 2; Length 246;  
Best Local Similarity 47.1%; Pred. No. 6.1;  
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQ 17  
||| |::| |::| |  
Db 33 NSSAEPSPETETNSPVAQ 49

RESULT 13  
T26968  
hypothetical protein Y47H9C.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T26968  
R:Harris, B.  
submitted to the EMBL Data Library, October 1998  
A:Reference number: Z20293  
A:Accession: T26968  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-394 <WIL>  
A:Cross-references: EMBL:AL032657; PIDN:CAA21735.1; GSPDB:GNO0019; CESP:Y47H9C.6  
C:Genetics:  
A:Gene: CESP:Y47H9C.6.  
A:Map position: 1  
A:Introns: 31/3; 46/1; 76/1; 92/1; 118/1; 156/1; 194/2; 287/3; 332/3; 347/1; 385/1

Query Match 50.5%; Score 46; DB 2; Length 394;  
Best Local Similarity 57.1%; Pred. No. 10;  
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 EKAPSATSSPVTQD 18  
:|::|::|::|::|  
Db 170 DPGTASSSPLTQD 183

RESULT 14  
T16057  
hypothetical protein F13D11.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 23-Mar-2001  
C:Accession: T16057  
R:Fulton, L.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid F13D11.  
A:Reference number: S69020  
A:Accession: T16057  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-908 <FUL>  
A:Cross-references: EMBL:U40939; NID:g1072175; PID:g1072177; PIDN:AAA81701.1; CESP:F13D11.2  
C:Genetics:  
A:Gene: CESP:F13D11.2  
A:Introns: 22/3; 168/3; 539/3; 729/1; 769/3; 839/3; 858/2

Query Match 48.4%; Score 44; DB 2; Length 908;  
Best Local Similarity 55.0%; Pred. No. 53;

Matches 11; Conservative 2; Mismatches 3; Indels 4; Gaps 1;  
QY 1 NNNVEKAP-----SATSSPVT 16  
||| |::| |::| |  
Db 189 NNNNEAPASTVSACSTPTT 208

RESULT 15  
T43676  
hunchback-related protein - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T43676  
R:Pay, D.S.; Stanley, H.M.; Han, M.; Wood, W.B.  
Dev. Biol. 205, 240-253, 1999  
A:Title: A Caenorhabditis elegans homologue of hunchback is required for late stages  
A:Reference number: Z22622; MUID:99117349  
A:Accession: T43676  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-982 <FAY>  
A:Cross-references: EMBL:AF097737; NID:g4323034; PIDN:AAD16170.1; PID:g4323035  
C:Genetics:  
A:Gene: hbl-1

Query Match 48.4%; Score 44; DB 2; Length 982;  
Best Local Similarity 55.0%; Pred. No. 57;  
Matches 11; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 1 NNNVEKAP-----SATSSPVT 16  
||| |::| |::| |  
Db 289 NNNNEAPASTVSACSTPTT 308

Search completed: September 10, 2001, 14:01:16  
Job time: 215 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2001, 14:00:25 ; Search time 67.08 Seconds  
(without alignments)  
16.268 Million cell updates/sec

Title: US-08-833-506c-32

Perfect score: 91

Sequence: 1 NNNVEKAPSATSSPVTQD 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

1:	/SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2:	/SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3:	/SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4:	/SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5:	/SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6:	/SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7:	/SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8:	/SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9:	/SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10:	/SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11:	/SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12:	/SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13:	/SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14:	/SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15:	/SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16:	/SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17:	/SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18:	/SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19:	/SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20:	/SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21:	/SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22:	/SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	91	100.0	18	AAW81207	Human iNOS peptide
2	91	100.0	18	AAW81211	Human iNOS peptide
3	86	94.5	18	AAW81175	Human iNOS (25-42)
4	86	94.5	18	AAW81277	Human iNOS peptide
5	86	94.5	1146	AAW96322	Inducible nitric o
6	86	94.5	1153	AAW55764	Sequence encoded b
7	86	94.5	1153	AAW55764	Nitric-oxide-synth
8	86	94.5	1153	AAW88464	Hepatocyte-inducib
9	86	94.5	1153	AAW36113	Human inducible ni
10	86	94.5	1153	AAW31724	Amino acid sequenc
11	86	94.5	1153	AAW66724	Human inducible ni

12	75	82.4	15	19	AAW81218	Human iNOS peptide
13	75	82.4	15	19	AAW81284	Human iNOS peptide
14	73	80.2	15	19	AAW81280	Human iNOS peptide
15	73	80.2	15	19	AAW81214	Human iNOS peptide
16	68	74.7	18	19	AAW81177	Rat iNOS (25-42) p
17	68	74.7	18	19	AAW81321	Human iNOS peptide
18	68	74.7	18	19	AAW81321	Rat iNOS peptide f
19	68	74.7	1147	17	AAW02571	Rat inducible nitr
20	62	68.1	18	19	AAW81320	Human iNOS peptide
21	62	68.1	18	19	AAW81312	Mouse iNOS peptide
22	60	65.9	12	19	AAW81219	Human iNOS peptide
23	60	65.9	12	19	AAW81285	Human iNOS peptide
24	59	64.8	12	19	AAW81281	Human iNOS peptide
25	59	64.8	12	19	AAW81215	Human iNOS peptide
26	57	62.6	18	19	AAW81176	Mouse iNOS (25-42)
27	57	62.6	1144	16	AAW77360	Inducible nitric o
28	57	62.6	1144	19	AAW51246	Inducible nitric o
29	47	51.6	9	19	AAW81220	Human iNOS peptide
30	47	51.6	9	19	AAW81226	Human iNOS peptide
31	44	48.4	9	19	AAW81216	Human iNOS peptide
32	44	48.4	9	19	AAW81282	Human iNOS peptide
33	44	48.4	504	21	AAW08720	Amino acid sequenc
34	44	48.4	537	21	AAW08719	Amino acid sequenc
35	44	48.4	563	21	AAW08721	Amino acid sequenc
36	44	48.4	573	21	AAW08722	Amino acid sequenc
37	44	48.4	596	21	AAW08715	Amino acid sequenc
38	43.5	47.8	3329	21	AAW56029	Human BRCA2 tumour
39	41	45.1	75	21	AAW01517	Human secreted pro
40	41	45.1	92	21	AAW76149	Human secreted pro
41	41	45.1	293	17	AAW04936	Chimeric endogluca
42	41	45.1	298	17	AAW04935	Chimeric endogluca
43	41	45.1	542	14	AAW38746	fySSRP. Saccharom
44	41	45.1	542	19	AAW39214	S. cerevisiae SSRP
45	41	45.1	1049	21	AAW42125	Human ORFX ORF1889

#### ALIGNMENTS

RESULT 1

AAW81207  
ID AAW81207 standard; peptide; 18 AA.

XX AAW81207;

XX 30-APR-1999 (first entry)

XX Human iNOS peptide fragment capable of binding Mab 21C10-ID10 #1.

XX Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis; Mab.

XX Homo sapiens.

XX W09845710-A1.

XX 15-OCT-1998.

XX 11-APR-1997; 97WO-US06500.

XX 07-APR-1997; 97US-6667777.

XX (WEBB/) WEBBER R.

XX Webber R;

XX WPI; 1998-594495/50.

XX Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.

```

XX PS Example 3; Page 32; 93pp; English.
XX CC This invention describes an immunoassay method where a sample with a
XX CC specific binding entity (e.g. a monoclonal antibody) reactive to human
XX CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
XX CC to detect the presence of human iNOS protein in the sample. The method
XX CC can be used for the detection and quantitation of human iNOS in cells and
XX CC tissues for various pathophysiological conditions such as sepsis, septic
XX CC shock, myocardial infarction, rejection of tissue in organs following
XX CC transplantation, monitoring "flare ups" in certain autoimmune diseases
XX CC such as lupus, psoriasis, and multiple sclerosis. This sequence
XX CC represents a peptide from human iNOS which is used in the method of the
XX CC invention.
XX SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18
Db 1 nnnvekapsatspvtqd 18

RESULT 2
AAW81211
ID AAW81211 standard; peptide; 18 AA.
AC AAW81211;
XX 30-APR-1999 (first entry)
DT Human iNOS peptide fragment PS-5103.
DE Inducible nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Modified-site 18
FT /note= "Asp residue amidated"
XX
XX WO9845710-A1.
XX 15-OCT-1998.
XX 11-APR-1997; 97WO-US06500.
XX 07-APR-1997; 97US-6667777.
XX (WEBB/) WEBBER R.
XX Webber R;
XX WPI; 1998-594495/50.
XX Detection of human inducible nitric oxide synthase - using an
XX immunoassay in which a sample is contacted with a specific binding
XX entity reactive with human iNOS or mimics.
XX Disclosure; Page 34; 93pp; English.
XX This invention describes an immunoassay method where a sample with a
XX specific binding entity (e.g. a monoclonal antibody) reactive to human
XX inducible nitric oxide synthase (iNOS) or mimics of this protein is used
XX to detect the presence of human iNOS protein in the sample. The method
XX can be used for the detection and quantitation of human iNOS in cells and
XX tissues for various pathophysiological conditions such as sepsis, septic
XX shock, myocardial infarction, rejection of tissue in organs following
XX CC transplantation, monitoring "flare ups" in certain autoimmune diseases
XX CC such as lupus, psoriasis, and multiple sclerosis. This sequence
XX CC represents a peptide from human iNOS which is used in the method
XX CC of the invention.
XX SQ Sequence 18 AA;

Query Match 100.0%; Score 91; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18
Db 1 nnnvekapsatspvtqd 18

RESULT 3
AAW81175
ID AAW81175 standard; peptide; 18 AA.
XX
XX AC AAW81175;
XX 30-APR-1999 (first entry)
DT Human iNOS (25-42) peptide fragment.
DE Inducible nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
XX Homo sapiens.
OS
XX WO9845710-A1.
XX 15-OCT-1998.
XX 11-APR-1997; 97WO-US06500.
XX 07-APR-1997; 97US-6667777.
XX (WEBB/) WEBBER R.
XX Webber R;
XX WPI; 1998-594495/50.
XX Detection of human inducible nitric oxide synthase - using an
XX immunoassay in which a sample is contacted with a specific binding
XX entity reactive with human iNOS or mimics.
XX Disclosure; Page 20; 93pp; English.
XX This invention describes an immunoassay method where a sample with a
XX specific binding entity (e.g. a monoclonal antibody) reactive to human
XX inducible nitric oxide synthase (iNOS) or mimics of this protein is used
XX to detect the presence of human iNOS protein in the sample. The method
XX can be used for the detection and quantitation of human iNOS in cells and
XX tissues for various pathophysiological conditions such as sepsis, septic
XX shock, myocardial infarction, rejection of tissue in organs following
XX CC transplantation, monitoring "flare ups" in certain autoimmune diseases
XX CC such as lupus, psoriasis, and multiple sclerosis. This sequence
XX CC represents a peptide fragment from human iNOS which is used in the method
XX CC of the invention.
XX SQ Sequence 18 AA;

Query Match 94.5%; Score 86; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 8.8e-07;

```

XX	28-JUN-1999	(first entry)
XX		
XX		Inducible nitric oxide synthase.
DE		
XX		
DE		
KW		Manganese containing superoxide dismutase; MnSOD; IDDM;
KW		diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell;
KW		fatty acid; lipotoxic; cytotoxic; cytokine; osteoporosis;
KW		inflammatory disease; autoimmune disease; neurodegenerative disease
XX		
OS		Homo sapiens.
XX		
PN	W09906059-A2.	
XX		
PD	11-FEB-1999.	
XX		
PF	30-JUL-1998;	98WO-US15781.
XX		
PR	03-MAR-1998;	98US-0055092.
XX		
PR	30-JUL-1997;	97US-0055092.
XX		
PA	(BETA-) BETAGENE INC.	
XX	(TEXA ) UNIV TEXAS SYSTEM.	
PA		
PI	Clark SA, Hohmeier H, Koyama K, Lee Y, Newgard CB;	
PI	Ohneda M, Shimabukuro, Thigpen A, Unger RH;	
PI		
DR	WPI: 1999-153448/13.	
DR	N-PSDB; AAX08434.	
XX		
PT	Protection of mammalian cells against immunotoxicity or lipotoxicity	
PT	- used for treating, e.g. diabetes, obesity, wasting syndromes,	
PT	osteoporosis, inflammatory diseases, autoimmune diseases or	
PT	neurodegenerative diseases	
XX		
PS	Disclosure; Page 247-251; 253pp; English.	
XX		
CC	Inhibition of cytokine mediated immunotoxicity of cells can be	
CC	achieved by blocking free radical production or the accumulation of	
CC	free radicals in that cell. Treatment of insulin dependent diabetes	
CC	mellitus (IDDM) can be achieved by blocking nitric oxide (NO)	
CC	production in a pancreatic beta cell and by providing a composition	
CC	comprising an agent that reduces levels of fatty acids in the cells	
CC	and protects beta-cells of the subject against lipid-mediated cell	
CC	death. Cells can also be protected against nitric oxide mediated	
CC	cytotoxicity by introducing into the cell an antioxidanting agent.	
CC	The methods can be used for protecting cells against immunotoxicity	
CC	mediated by, e. g. IL-1 beta, IL-1 alpha, gamma IFN, TNF alpha, TNF	
CC	beta, IL-8, IL-2, IL-6, IL-3, IL-5, IL-7, IL-9, IL-14, IL-17,	
CC	granulocyte-macrophage colony stimulating factor or monocyte	
CC	chemoattractant protein-1. The methods can be used for the treatment	
CC	of e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity	
CC	wasting syndromes, short stature, osteoporosis, inflammatory	
CC	diseases, autoimmune diseases, or neurodegenerative diseases.	
XX		
SQ	Sequence	1146 AA;
	Query Match	94.5%; Score 86; DB 20; Length 1146;
	Best Local Similarity	94.4%; Pred. No. 0.0001;
	Matches 17; Conservative	0; Mismatches 1; Indels 0; Gaps
QY	1 NNNVEKAPSSPVTQD 18	
Db	25 nnnvekapsctspvtqd 42	
RESULT	6	
AAR55764		
ID	AAR55764 standard; Protein: 1153 AA.	
XX		
AC	AAR55764;	
XX		

DT 28-DEC-1994 (first entry)  
 XX Sequence encoded by the cDNA clone for human hepatocyte inducible  
 DE nitric oxide synthase.  
 DE  
 XX Nitric oxide synthase; hepatocyte; hypotensive shock; therapy.  
 KW  
 XX Homo sapiens.  
 OS  
 PN WO9412645-A.  
 XX  
 PD 09-JUN-1994.  
 XX  
 XX 23-NOV-1993; 93WO-US11401.  
 PF  
 XX 25-NOV-1992; 92US-0981344.  
 PR  
 XX (UYPI-) UNIV PITTSBURGH.  
 PA  
 XX Billiar TR, Geller DA, Nussler AK, Simmons RL;  
 PI  
 XX WPI; 1994-200273/24.  
 DR  
 DR N-PSDB; AAQ66914.  
 XX  
 XX cDNA clone encoding human inducible nitric oxide synthase - used  
 PT to prevent the hypotensive shock seen with sepsis  
 PT  
 XX  
 XX Disclosure; Fig 1; 53pp; English.  
 PS  
 XX AAQ66914 is from human hepatocyte inducible nitric oxide synthase cDNA  
 CC clone pHINOS from lambda Zap II cDNA library. The original source  
 CC was induced human hepatocyte RNA. HINOS cDNA plasmid is pref.  
 CC transformed in E. coli SOLR (ATCC 69126). The inventors claim a  
 CC clone with the cDNA sequence in AAQ66914 and a cDNA clone which  
 CC encodes AAR55764. The cloning and expression of a human tissue nitric  
 CC oxide synthase cDNA provides a source of the enzyme for therapeutic  
 CC purposes, for example to prevent the hypotensive shock seen with  
 CC sepsis.  
 CC  
 XX  
 XX Sequence 1153 AA;  
 SQ  
  
 Query Match 94.5%; Score 86; DB 15; Length 1153;  
 Best Local Similarity 94.4%; Pred. No. 0.0001;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 1 NNNVEKAPSATSSPVTQD 18  
 Db ||||||| |||||||  
 25 nnnvekapcatsspvtqd 42  
  
 RESULT 7  
 AAR63206  
 ID AAR63206 standard; Protein; 1153 AA.  
 XX  
 AC AAR63206;  
 XX  
 DT 09-MAY-1995 (first entry)  
 XX  
 DE Nitric-oxide-synthase.  
 XX  
 KW Nitric-oxide-synthase; NO-synthase; NOS; chondrocyte;  
 KW interleukin-1-beta; pBSHSINOS; arthritis; hypertension;  
 KW septic shock; inflammation; ischemia; dementia; obesity; tumor;  
 KW agonist; antagonist; vector; CHO; Chinese hamster ovary;  
 KW cell culture.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9423038-A.  
 XX  
 PD 13-OCT-1994.  
 XX

PF 25-MAR-1994; 94WO-GB00621.  
 XX  
 PR 26-MAR-1993; 93GB-0006386.  
 XX  
 PA (WELL ) WELLCOME FOUND LTD.  
 XX  
 PI Charles IG, Moncada SE, Palmer RMJ, Moncada S;  
 XX  
 DR WPI; 1994-333198/41.  
 DR N-PSDB; AAQ77700.  
 XX  
 XX New human inducible nitric oxide synthase - useful for  
 PT identifying enzyme inhibitors and stimulators, and for diagnosis  
 PT and treatment of e.g. viral infections or tumours  
 PT  
 XX Disclosure; Page 25-31; 42pp; English.  
 PS  
 XX Human chondrocytes were incubated with interleukin-1-beta to induce  
 CC nitric-oxide-synthase. cDNA was generated and used to construct a  
 CC library in lambda ZAPII. This was screened with a 650 bp fragment of  
 CC mouse inducible NO-synthase cDNA to identify the full-length clone  
 CC pBSHSINOS. The insert was transferred to pSVL to give a vector  
 CC capable of expressing NO-synthase in CHO cells under control of a  
 CC heterologous constitutive promoter.  
 CC  
 XX Sequence 1153 AA;  
 SQ  
  
 Query Match 94.5%; Score 86; DB 15; Length 1153;  
 Best Local Similarity 94.4%; Pred. No. 0.0001;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 1 NNNVEKAPSATSSPVTQD 18  
 Db ||||||| |||||||  
 25 nnnvekapcatsspvtqd 42  
  
 RESULT 8  
 AAR88464  
 ID AAR88464 standard; Protein; 1153 AA.  
 XX  
 AC AAR88464;  
 XX  
 DT 13-MAY-1996 (first entry)  
 XX  
 DE Hepatocyte inducible nitric oxide synthase.  
 XX  
 DE Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy;  
 KW vascular occlusive disease; cancer; infection.  
 KW  
 KW Homo sapiens.  
 OS  
 XX WO9600006-A1.  
 PN  
 XX 04-JAN-1996.  
 PD  
 XX 20-JUN-1995; 95WO-US07849.  
 PF  
 XX 24-JUN-1994; 94US-0265046.  
 PR  
 XX (UYPI-) UNIV PITTSBURGH.  
 PA  
 XX Billiar TR, Geller DA, Nussler AK, Simmons RL, Tzeng E;  
 PI  
 XX WPI; 1996-068641/07.  
 DR  
 DR N-PSDB; AAT10115.  
 XX  
 XX Inducible nitric oxide synthase gene - useful in gene therapy to  
 PT treat, e.g. vascular occlusive disease and cancer  
 PT  
 XX Disclosure; Page 54-58; 91pp; English.  
 PS  
 XX An inducible nitric oxide synthase (iNOS = AAR88464) is the product  
 CC



CC of a cDNA clone (AAT10115) derived from human hepatocytes induced  
 CC for iNOS biosynthesis. The iNOS can be obtd. by expression of  
 CC the cDNA e.g. in mammalian host cells and is used in the  
 CC development of selective inhibitors of NOS or to treat diseases  
 CC affected by nitric oxide.

XX SQ Sequence 1153 AA;

Query Match 94.5%; Score 86; DB 17; Length 1153;  
 Best Local Similarity 94.4%; Pred. No. 0.0001;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18  
 DB 25 nnnvekpcatsspvtqgd 42

RESULT 9

AAW36113  
 ID AAW36113 standard; Protein; 1153 AA.

XX AC AAW36113;

DT 11-MAY-1998 (first entry)

XX Human inducible nitric oxide synthetase.

XX Nitric oxide synthetase; NOS; iNOS; HPI NOS; human;  
 KW erectile dysfunction; impotence; gene therapy; corpora cavernosa;  
 KW relaxant.

XX OS Homo sapiens.

XX PN WO9742965-A1.

XX PD 20-NOV-1997.

XX PF 09-MAY-1997; 97WO-US07643.

XX PR 10-MAY-1996; 96US-0017373.

XX PA (GONZ/) GONZALEZ-CADAVID N F.

XX PA (RAJF/) RAJFER J.

XX PI Gonzalez-Cadavid NF, Rajfer J;

XX DR WPI; 1998-008577/01.

XX DR N-PSDB; AAT98199.

XX Treatment of erectile dysfunction - by introducing an agent into  
 PT penile tissue, particularly for inducing cavernosal smooth muscle  
 PT relaxation or increasing NOS levels

XX PS Claim 12; Page 38-41; 53pp; English.

XX This protein comprises human penis inducible nitric oxide  
 CC synthetase (HPI NOS). Its amino acid sequence was deduced from a  
 CC cDNA clone (see AAT98199) derived from human penile smooth muscle  
 CC cell mRNA. The invention is directed to a method of treating  
 CC erectile dysfunction in a patient by providing an agent capable of  
 CC treating erectile dysfunction, and introducing an effective amount  
 CC of the agent into the penile tissue of the patient. Preferably,  
 CC the agent induces cavernosal smooth muscle relaxation, and/or  
 CC produces an increase in the level of NOS in tissue. Preferably,  
 CC the NOS is iNOS, and the agent is introduced into the corpora  
 CC cavernosa of the penis. The agent is preferably an NOS inducer, an  
 CC NOS protein such as HPI NOS, a cDNA encoding an NOS such as HPI NOS,  
 CC or cDNA transformed penile cells, especially corpora cavernosa  
 CC cells.

XX SQ Sequence 1153 AA;

Query Match 94.5%; Score 86; DB 19; Length 1153;  
 Best Local Similarity 94.4%; Pred. No. 0.0001;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18  
 DB 25 nnnvekpcatsspvtqgd 42

RESULT 10

AAB31724  
 ID AAB31724 standard; Protein; 1153 AA.

XX AC AAB31724;

XX DT 30-APR-2001 (first entry)

XX Amino acid sequence of a human inducible nitric oxide synthase (NOS).

XX Gene therapy; angiogenesis; nucleic acid delivery; arteriosclerosis;  
 KW nitric oxide synthase; NOS; endothelial dysfunction.

XX OS Homo sapiens.

XX PN WO200103728-A2.

XX PD 18-JAN-2001.

XX PF 07-JUL-2000; 2000WO-NL00482.

XX PR 09-JUL-1999; 99EP-0202263.

XX PR 09-JUL-1999; 99US-0143101.

XX PA (INTR-) INTROGENE BV.

XX PI Vogels R, Verlinden SFF;

XX DR WPI; 2001-123142/13.

XX Nucleic acid delivery vehicle comprising a nucleic acid encoding nitric  
 PT oxide synthase, used for isolated tissue perfusion treatment to enhance  
 PT and induce angiogenesis -

XX PS Disclosure; Fig 6; 37pp; English.

XX The specification describes a method for gene therapy for enhancing  
 CC and inducing angiogenesis. The method uses a nucleic acid delivery  
 CC vehicle, which comprises a nucleic acid encoding nitric oxide synthase  
 CC (NOS). The delivery vehicle is used for the manufacture of a  
 CC pharmaceutical composition for isolated tissue perfusion treatment.  
 CC The method is useful for enhancing and/or inducing angiogenesis in  
 CC patients with endothelial dysfunctions, in particular arteriosclerosis.  
 CC The present sequence represents an inducible NOS.

XX SQ Sequence 1153 AA;

Query Match 94.5%; Score 86; DB 22; Length 1153;  
 Best Local Similarity 94.4%; Pred. No. 0.0001;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSSPVTQD 18  
 DB 25 nnnvekpcatsspvtqgd 42

RESULT 11

AAB66724  
 ID AAB66724 standard; protein; 1153 AA.

XX AC AAB66724;

XX XX

```

DT 09-APR-2001 (first entry)
DE Human inducible nitric oxide synthase.
KW Nitric oxide synthase; NOS; angiogenesis; gene therapy.
XX
OS Homo sapiens.
PN EP1067190-A1.
PD 10-JAN-2001.
XX
PF 09-JUL-1999; 99EP-0202263.
XX
PR 09-JUL-1999; 99EP-0202263.
XX
PA (INTR-) INTROGENE BV.
XX
PI Vogels R, Verlinden S;
XX
DR WPI; 2001-125729/14.
XX
PT Use of a nucleic acid delivery vehicle comprising a nucleic acid
PT encoding nitric oxide synthase, especially useful in gene therapy for
PT enhancing and/or inducing angiogenesis and treating atherosclerosis.
XX
PS Examples; Page 14-18; 39pp; English.
XX
CC The present invention relates to use of a nucleic acid delivery
CC vehicle comprising a nucleic acid encoding nitric oxide synthase
CC (NOS) activity for the manufacture of a composition for essentially
CC isolated tissue perfusion treatment to enhance and/or induce
CC angiogenesis. The nucleic acid delivery vehicle is particularly
CC useful in gene therapy for the treatment of atherosclerosis.
XX
SQ Sequence 1153 AA;

Query Match 94.5%; Score 86; DB 22; Length 1153;
Best Local Similarity 94.4%; Pred. No. 0.0001;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSPVTQD 18
Db 25 nnnvekapsatpsvtqd 42
||||||| |||||||

RESULT 12
AAW81218
ID AAW81218 standard; peptide; 15 AA.
XX
AC AAW81218;
XX
DT 30-APR-1999 (first entry)
XX
DE Human iNOS peptide fragment PS-5247.
XX
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 15
FT /note="Val residue amidated"
XX
PN WO9845710-A1.
XX
PD 15-OCT-1998.
XX
PF 11-APR-1997; 97WO-US06500.

```

```

XX
PR 07-APR-1997; 97US-6667777.
XX
PA (WEBB/) WEBBER R.
XX
PI Webber R;
XX
DR WPI; 1998-594495/50.
XX
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
XX
PS Example 4; Page 35; 93pp; English.
XX
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention.
XX
SQ Sequence 15 AA;

Query Match 82.4%; Score 75; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNNVEKAPSATSPV 15
Db 1 nnnvekapsatsspv 15
||||||| |||||||

RESULT 13
AAW81284
ID AAW81284 standard; peptide; 15 AA.
XX
AC AAW81284;
XX
DT 30-APR-1999 (first entry)
XX
DE Human iNOS peptide fragment for epitope mapping #5.
XX
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis; epitope mapping.
XX
OS Homo sapiens.
XX
PN WO9845710-A1.
XX
PD 15-OCT-1998.
XX
PF 11-APR-1997; 97WO-US06500.
XX
PR 07-APR-1997; 97US-6667777.
XX
PA (WEBB/) WEBBER R.
XX
PI Webber R;
XX
DR WPI; 1998-594495/50.
XX
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.

```

XX PS Example 4; Fig 7A; 93pp; English.  
XX CC This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathophysiological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
CC invention.  
XX SQ Sequence 15 AA;  
Query Match 82.4%; Score 75; DB 19; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NNNVEKAPSATSPV 15  
Db 1 nnnvekapsatspv 15  
IIIIIIIIIIIIIIII  
RESULT 14  
AAW81280  
ID AAW81280 standard; peptide; 15 AA.  
XX AC AAW81280;  
XX 30-APR-1999 (first entry)  
XX Human iNOS peptide fragment for epitope mapping #1.  
XX Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis; epitope mapping.  
XX OS Homo sapiens.  
XX WO9845710-A1.  
XX 15-OCT-1998.  
XX 11-APR-1997; 97WO-US06500.  
XX 07-APR-1997; 97US-6667777.  
XX (WEBB/) WEBBER R.  
XX Webber R;  
XX WPI; 1998-594495/50.  
XX Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
XX Example 4; Fig 7A; 93pp; English.  
XX This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathophysiological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence

CC represents a peptide from human iNOS which is used in the method of the  
CC invention.  
XX SQ Sequence 15 AA;  
Query Match 80.2%; Score 73; DB 19; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.6e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 VEKAPSATSPVTQD 18  
Db 1 vekapsatsspvtqd 15  
IIIIIIIIIIIIIIII  
RESULT 15  
AAW81214  
ID AAW81214 standard; peptide; 15 AA.  
XX AC AAW81214;  
XX 30-APR-1999 (first entry)  
XX Human iNOS peptide fragment PS-5243.  
XX Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;  
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;  
KW myocardial infarction; tissue rejection; transplantation; psoriasis;  
KW autoimmune disease; multiple sclerosis.  
XX OS Homo sapiens.  
XX Key Location/Qualifiers  
FH Modified-site 15  
FT /note= "Asp residue amidated"  
XX WO9845710-A1.  
XX 15-OCT-1998.  
XX 11-APR-1997; 97WO-US06500.  
XX 07-APR-1997; 97US-6667777.  
XX (WEBB/) WEBBER R.  
XX Webber R;  
XX WPI; 1998-594495/50.  
XX Detection of human inducible nitric oxide synthase - using an  
PT immunoassay in which a sample is contacted with a specific binding  
PT entity reactive with human iNOS or mimics.  
XX Example 4; Page 34; 93pp; English.  
XX This invention describes an immunoassay method where a sample with a  
CC specific binding entity (e.g. a monoclonal antibody) reactive to human  
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used  
CC to detect the presence of human iNOS protein in the sample. The method  
CC can be used for the detection and quantitation of human iNOS in cells and  
CC tissues for various pathophysiological conditions such as sepsis, septic  
CC shock, myocardial infarction, rejection of tissue in organs following  
CC transplantation, monitoring "flare ups" in certain autoimmune diseases  
CC such as lupus, psoriasis, and multiple sclerosis. This sequence  
CC represents a peptide from human iNOS which is used in the method of the  
CC invention.  
XX SQ Sequence 15 AA;  
Query Match 80.2%; Score 73; DB 19; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.6e-05;

Matches	15;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	4	VEKAPSATSSPVTQD	18						
Db	1	vekapsatsspvtqd	15						

Search completed: September 10, 2001, 14:00:25  
Job time: 169 sec